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(54) Title: *PLASMODIUM FALCIPARUM* ANTIGENS AND METHODS OF USE

(57) Abstract: The subject invention provides novel *Plasmodium falciparum*antigens and novel polynucleotides encoding these antigens. Also provided by the subject invention are methods of using these antigens and polynucleotides.

DESCRIPTION

PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF USE

The subject invention was made with government support under a research project supported by Grant No. 1 R43AI49051-01 NIAID.

Cross Reference to Related Application

[0001] This application claims the benefit of U.S. Provisional Application 60/431,494, filed December 6, 2002, which is hereby incorporated by reference in its entirety, including all drawings and tables.

Background of Invention

[0002] The recent explosion in genomic sequencing has deposited a wealth of information in the hands of researchers. However, there is not yet a means to efficiently analyze such data to identify which antigens among many thousands are appropriate targets for vaccine development.

[0003] More than 5000 proteins are expressed during the life cycle of the *Plasmodium* spp. parasite. Subunit vaccines currently in development are based on a single or few antigens and may therefore, elicit too narrow a breadth of response, providing neither optimal protection nor protection on genetically diverse backgrounds. By contrast, to duplicate the protection induced by whole organism vaccination (Good, M.F. & Doolan, D.L. Immune effector mechanisms in malaria. *Curr. Opin. Immunol.* 11, 412-419 (1999)), a malaria vaccine targeting an unprecedented number of parasite-derived proteins through inclusion of their minimal $CD8^+$ and $CD4^+$ T cell epitopes in a multiepitope construct appears to be required. However, the antigens mediating whole organism induced protection are largely unknown.

[0004] Because of various factors, principally related to antigen abundance and immunodominance, not all possible antigens are recognized by natural immunity (Yewdell JW, Bennink JR. Immunodominance in major histocompatibility complex class

I-restricted T lymphocyte responses. *Annu. Rev. Immunol.* **17**, 51-88. (1999)). Various approaches have been proposed for antigen identification, including expression cloning (Kawakami, Y. & Rosenberg, S. A. Immunobiology of human melanoma antigens MART-1 and gp100 and their use for immuno-gene therapy. *Int. Rev. Immunol.* **14**, 173-192 (1997)), elution and mass spectrometry sequencing of naturally processed MHC-bound peptides (Rotzschke, O. *et al.* Isolation and analysis of naturally processed viral peptides as recognized by cytotoxic T cells. *Nature* **348**, 252-254 (1990); van Bleek, G. M. & Nathenson, S. G. Isolation of an endogenously processed immunodominant viral peptide from the class I H-2Kb molecule. *Nature* **348**, 213-216 (1990); Hunt, D. F. *et al.* Peptides presented to the immune system by the murine class II major histocompatibility complex molecule I-Ad. *Science* **256**, 1817-1820 (1992); Cox, A. L. *et al.* Identification of a peptide recognized by five melanoma-specific human cytotoxic T cell lines. *Science* **264**, 716-719 (1994)), *in vitro* testing of pools of overlapping peptides (Kern, F. *et al.* Cytomegalovirus (CMV) Phosphoprotein 65 Makes a Large Contribution to Shaping the T Cell Repertoire in CMV-Exposed Individuals. *J. Infect. Dis.* **185**, 1709-1716 (2002)), and reverse immunogenetics (Davenport, M. P. & Hill, A. V. Reverse immunogenetics: from HLA-disease associations to vaccine candidates. *Mol. Med. Today* **2**, 38-45 (1996); Aidoo, M. *et al.* Identification of conserved antigenic components for a cytotoxic T lymphocyte-inducing vaccine against malaria. *Lancet* **345**, 1003-1007 (1995)). However, these methods suffer from potential problems such as the repeated identification of the same (frequent/dominant) epitope, biases at the level of expansion of T cell populations, and use of clonal/oligoclonal T cells. They also tend to underestimate the complexity of responses, and are not able to analyze a large number of potential targets in the context of multiple HLA types. Finally, none of these approaches easily lends itself towards the daunting task of efficiently analyzing large amounts of genomic sequence data.

Brief Summary

[0005] The subject invention also provides novel *Plasmodium falciparum* antigens that are useful in therapeutic and diagnostic applications. In various aspects, the subject invention provides embodiments such as:

A) isolated and/or purified polynucleotide sequences comprising:

a) a polynucleotide sequence encoding a polypeptide sequence selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27;

b) a complementary polynucleotide sequence to a polynucleotide sequence encoding a polypeptide sequence selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27;

c) a polynucleotide sequence having at least about 20% to 99.99% identity to a polynucleotide sequence of A(a) or A(b);

d) a fragment of a polynucleotide sequence according to A(a) or A(b);

e) a polynucleotide sequence encoding a polypeptide as set forth in Table 2, 3, 4, 5, or 6, or a polynucleotide sequence encoding a polypeptide selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27;

f) a polynucleotide sequence encoding a variant of a polypeptide (*e.g.*, a variant polypeptide) selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27;

g) a polynucleotide sequence encoding a polypeptide fragment of a polypeptide selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27, wherein the fragment has substantially the same serologic reactivity as the native polypeptide and/or substantially the same T-cell reactivity as the native polypeptide or fragment;

h) a polynucleotide sequence encoding a fragment of a variant polypeptide of a polypeptide selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27, wherein the fragment of the variant polypeptide has substantially the same serologic activity as the native polypeptide or substantially the same T-cell reactivity as the native polypeptide or fragment; or

i) a polynucleotide sequence encoding a multi-epitope construct;

B) primers or detection probes (*e.g.*, fragments of the disclosed polynucleotide sequences) for hybridization with a target sequence or the amplicon generated from the target sequence comprising a sequence of at least 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 consecutive nucleotides of the polynucleotide sequences set forth herein. Labeled probes or primers are labeled with a radioactive compound or with another type of label as set forth in embodiment C, below;

C) isolated polynucleotides according to embodiments A or B further comprising a label; labels can include, and are not limited to 1) radioactive labels, 2) enzyme labels, 3) chemiluminescent labels, 4) fluorescent labels, 5) magnetic labels, or other suitable labels. Exemplary labels include, and are not limited to, ^{32}P, ^{35}S, ^{3}H, ^{125}I, biotin, acetylaminofluorene, digoxigenin, 5-bromo-deoxyuridine, or fluorescein;

D) methods of detecting *P. falciparum* in biological samples comprising contacting a biological sample with isolated polynucleotides of embodiments A, B, or C. In this embodiment, *P. falciparum* cells, or cells comprising (infected) by *P. falciparum* are recovered, lysed, and DNA and/or RNA are extracted from the lysed cells. The extracted DNA or RNA is then tested using polynucleotides and/or probes set forth herein for the presence of *P. falciparum*. Typical assay formats utilizing nucleic acid hybridization includes, and are not limited to, 1) nuclear run-on assay, 2) slot blot assay, 3) northern blot assay (Alwine, *et al.* Proc. Natl. Acad. Sci. 74:5350), 4) magnetic particle separation, 5) nucleic Acid or DNA chips, 6) reverse Northern blot assay, 7) dot blot assay, 8) in situ hybridization, 9) RNase protection assay (Melton, *et al.* Nuc. Acids Res. 12:7035 and as described in the 1998 catalog of Ambion, Inc., Austin, Tex.), 10) ligase chain reaction, 11) polymerase chain reaction (PCR), 12) reverse transcriptase (RT)-PCR (Berchtold, *et al.* Nuc. Acids. Res. 17:453), 13) differential display RT-PCR (DDRT-PCR) or other suitable combinations of techniques and assays;

E) analytical systems, such as DNA chips comprising polynucleotide sequences according to embodiments A, B, or C;

F) modified polynucleotide sequences comprising polynucleotide sequences according to embodiments A or B;

G) a polynucleotide sequence according to embodiments A, B, or F, further comprising regulatory sequences, such as promoters, enhancer elements, or termination sequences, that are operably linked to the polynucleotide sequences of embodiments A or B;

H) a vector comprising a promoter operably linked to a nucleic acid sequence of the subject invention (*e.g.*, as set forth in embodiments A, B, or F), optionally, one or more origins of replication, and, optionally, one or more selectable markers (*e.g.*, an antibiotic resistance gene);

I) host cells transformed by a vector according embodiment G or H. The host cell may be chosen from eukaryotic or prokaryotic systems, such as for example bacterial cells, (Gram negative or Gram positive), yeast cells, animal cells (such as Chinese hamster ovary (CHO) cells), plant cells, and/or insect cells using baculovirus vectors. In some embodiments, the host cells for expression of the polypeptides include, and are not limited to, those taught in U.S. Patent Nos. 6,319,691, 6,277,375, 5,643,570, or 5,565,335, each of which is incorporated by reference in its entirety, including all references cited within each respective patent.

I) novel compositions comprising a pharmaceutically acceptable carrier and a polynucleotide according to embodiments A or B;

J) methods of inducing an immune response or protective immune response in an individual comprising the administration of a composition comprising a polynucleotide according to embodiments A and/or B and a

pharmaceutically acceptable carrier in an amount sufficient to induce an immune response;

K) the method according to embodiment J, further comprising the administration of: 1) a viral vector comprising a polynucleotide according to embodiment A and/or B (or composition comprising the viral vector); and/or 2) a polypeptide antigen (or composition thereof) of the invention; in a preferred embodiment, the antigen is the polypeptide that is encoded by the polynucleotide administered as the polynucleotide vaccine. As a particularly preferred embodiment, the polypeptide antigen is administered as a booster subsequent to the initial administration of the polynucleotide vaccine. Exemplary viral vectors suitable for use in this embodiment include, but are not limited to, poxvirus such as vaccinia virus, avipox virus, fowlpox virus, a highly attenuated vaccinia virus (such as Ankara or MVA [Modified Vaccinia Ankara]), retrovirus, adenovirus, baculovirus and the like. In a preferred embodiment, the viral vector is Ankara or MVA;

L) compositions comprising the polynucleotides of embodiments A, B, or F inserted into nucleic acid vaccine vectors (plasmids) or viral vectors and, optionally, a pharmaceutically acceptable carrier, *e.g.*, saline;

M) one or more isolated polypeptides comprising:

a) a polypeptide encoded by a polynucleotide sequence according to embodiment A(a);

b) a variant polypeptide encoded by a polynucleotide sequence having at least about 20% to 99.99% identity to a polynucleotide according to embodiment A(a);

c) a fragment of a polypeptide or a variant polypeptide, wherein said fragment or variant has substantially the same serologic reactivity or substantially the same T-cell reactivity as the native polypeptide (*e.g.*, those polypeptides set forth in SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27 and Tables 2, 3, 4, 5 or 6);

d) a polypeptide sequence provided in Tables 2, 3, 4, 5 or 6 or selected from the group consisting of SEQ ID NO: NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27;

e) a variant polypeptide having at least about 20% to 99.99% identity to a polypeptide provided in Tables 2, 3, 4, 5 or 6 or selected from the group consisting of SEQ ID NO: NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27;

f) a polypeptide (epitope) set forth in Table 2, 3, 4, 5 or 6; or

g) a multi-epitope construct: 1) comprising at least one epitope set forth in Table 2, 3, 4, 5 or 6; 2) comprising a polypeptide selected from the group consisting of SEQ ID NO: NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27 and at least one epitope set forth in Tables 2, 3, 4, 5 and/or 6; or 3) comprising and at least one epitope set forth in Tables 2, 3, 4, 5 and/or 6 and one or more polypeptide selected from the group consisting of SEQ ID NO: NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27;

N) a polypeptide epitope according to embodiment M(f), wherein the polypeptide epitope is a CTL-inducing peptides of about 13 residues or less in length, preferably between about 8 and about 11 residues (*e.g.*, 8, 9, 10 or all residues), and more preferably 9 or 10 residues;

O) a polypeptide epitope according to embodiment M(f), wherein the polypeptide epitope is a HTL-inducing peptide of less than about 50 residues, preferably, between about 6 and about 30 residues, more preferably, between about 12 and 25 residues (*e.g.*, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 residues), and most preferably, between about 15 and 20 residues (*e.g.*, 15, 16, 17, 18, 19, or 20 residues);

P) methods for eliciting an immune response in an individual comprising the administration of compositions comprising polypeptides according

to embodiment M or N to an individual in amounts sufficient to induce an immune response in the individual;

Q) a composition comprising a pharmaceutically acceptable carrier and a polypeptide according to embodiment M or N, that can, optionally, contain an adjuvant;

R) diagnostic assays based upon Western blot formats, or standard immunoassays known to the skilled artisan, comprising contacting a biological sample obtained from an individual with a polypeptide according to the embodiments M or N and detecting the formation of an antibody-antigen complex or detecting the stimulation of T-cells obtained from the individual (for example, as set forth in the Examples herein);

S) a "multi-epitope construct" comprising: 1) polynucleotides that encode multiple polypeptide epitopes (of any length) that can bind to one or more molecules functioning in the immune system; or 2) polypeptides comprising multiple polypeptide epitopes that can bind to one or more molecules functioning in the immune system. Some embodiments provide for "multi-epitope constructs" that comprise a combination or series of different epitopes, optionally connected by "flanking" residues. "Multi-epitope constructs" can include the full length polypeptides from which the epitopes are obtained (*e.g.*, the polypeptides of SEQ ID NOs: 1-27);

T) a multi-epitope construct according to embodiment S, wherein the epitopes used in the formation of the multi-epitope construct are selected from those set forth in Table 2, Table, 3, Table 4, Table 5, and Table 6;

U) a multi-epitope construct according to embodiments S or T that is of "high affinity" or "intermediate affinity";

V) a multi-epitope construct according to embodiments S, T, or U that comprises five or more, ten or more, fifteen or more, twenty or more, or twenty-

five or more epitopes. Other embodiments provide multi-epitope constructs that comprise at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99 epitopes.

W) a multi-epitope construct according to embodiments S, T, U, or V wherein: a) all of the epitopes in a multi-epitope construct are from one organism (*e.g.*, the epitopes are obtained from *P. falciparum*); or b) or the multi-epitope construct includes epitopes present in two or more different organisms (*e.g.*, some epitopes from *P. falciparum* and some epitopes from another organism). Additionally, the same epitope may be present in a multi-epitope construct at more than one location in the construct. In some embodiments, novel epitopes of the subject invention may be linked to known epitopes of an organism (*e.g., P. falciparum* or another organism).

X) a multi-epitope construct according to embodiments S, T, U, V, or W, wherein the individual epitopes interact with an antigen binding site of an antibody molecule or fragment thereof, a class I HLA, a T-cell receptor, and/or a class II HLA molecule.

Y) a multi-epitope construct according to embodiments S, T, U, V, W, or X, wherein the construct further comprises, optionally, 1 to 5 "flanking" or "linking" residues positioned next to one or more epitopes;

Z) a multi-epitope construct according to embodiments S, T, U, V, W, X, or Y that has, optionally, been "optimized";

AA) an isolated antibody or fragment thereof that specifically binds to a polypeptide as set forth in embodiments M or N;

BB) a viral vector comprising a polynucleotide according to embodiment A or B. Exemplary viral vectors suitable for use in this embodiment include, but are not limited to, poxvirus such as vaccinia virus, avipox virus, fowlpox virus, a highly attenuated vaccinia virus (such as Ankara or MVA [Modified Vaccinia Ankara]), retrovirus, adenovirus, baculovirus and the like. In a preferred embodiment, the viral vector is Ankara or MVA; and/or

CC) a viral vector according to embodiment BB, wherein the viral vector further comprises nucleic acids encoding immunostimulatory molecules such as IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-15, Il-16, Il-18, IL-23, IL-24, erythropoietin, G-CSF, M-CSF, platelet derived growth factor (PDGF), MSF, FLT-3 ligand, EGF, fibroblast growth factor (FGF; *e.g.*, aFGF (FGF-1), bFGF (FGF-2), FGF-3, FGF-4, FGF-5, FGF-6, or FGF-7), insulin-like growth factors (*e.g.*, IGF-1, IGF-2); vascular endothelial growth factor (VEGF); interferons (*e.g.*, IFN-γ, IFN-α, IFN-β); leukemia inhibitory factor (LIF); ciliary neurotrophic factor (CNTF); oncostatin M; stem cell factor (SCF); transforming growth factors (*e.g.*, TGF-α, TGF-β1, TGF-β1, TGF-β1), or chemokines (such as, but not limited to, BCA-1/BLC-1, BRAK/Kec, CXCL16, CXCR3, ENA-78/LIX, Eotaxin-1, Eotaxin-2/MPIF-2, Exodus-2/SLC, Fractalkine/Neur7otactin, GROalpha/MGSA, HCC-1, I-TAC, Lymphotactin/ATAC/SCM, MCP-1/MCAF, MCP-3, MCP-4, MDC/STCP-1, ABCD-1, MIP-1α, MIP-1β, MIP-2α/GROβ, MIP-3α/Exodus/LARC, MIP-3β/Exodus-3/ELC, MIP-4/PARC/DC-CK1, PF-4, RANTES, SDF1α, TARC, or TECK).

Brief Description of Drawings and Tables

[0006] Table 1 presents a summary of immune reactivities of a panel of 27 novel antigens and four known antigens.

[0007] Tables 2-6 provide peptide epitopes of *P. falciparum*.

Brief Description of Sequences

[0008] Sequence ID NOs: 1-27 are amino acid sequences of novel malaria antigens.

Detailed Disclosure

[0009] The subject invention provides isolated and/or purified novel *P. falciparum* polynucleotides and fragments of these novel polynucleotides. Thus, the present invention provides isolated and/or purified polynucleotide sequences comprising:

a) a polynucleotide sequence encoding a polypeptide sequence selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27;

b) a complementary polynucleotide sequence to a polynucleotide sequence encoding a polypeptide sequence selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27;

c) a polynucleotide sequence having at least about 20% to 99.99% identity to a polynucleotide sequence of (a) or (b);

d) a fragment of a polynucleotide sequence according to (a) or (b);

e) a polynucleotide sequence encoding a polypeptide as set forth in Table 2, 3, 4, 5 or 6 or a polynucleotide sequence encoding a polypeptide selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27;

f) a polynucleotide sequence encoding variant of a polypeptide (*e.g.*, a variant polypeptide) selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27;

g) a polynucleotide sequence encoding a polypeptide fragment of a polypeptide selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27, wherein the fragment has substantially the same serologic reactivity as the native polypeptide or

substantially the same T-cell reactivity as the native polypeptide or fragment;

h) a polynucleotide sequence encoding a fragment of a variant polypeptide of a polypeptide selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27, wherein the fragment of the variant polypeptide has substantially the same serologic activity as the native polypeptide or substantially the same T-cell reactivity as the native polypeptide or fragment; or

i) a polynucleotide sequence encoding a multi-epitope construct.

[0010] "Nucleotide sequence", "polynucleotide" or "nucleic acid" can be used interchangeably and are understood to mean, according to the present invention, either a double-stranded DNA, a single-stranded DNA or products of transcription of the said DNAs (*e.g.*, RNA molecules). It should also be understood that the present invention does not relate to genomic polynucleotide sequences of *P. falciparum* in their natural environment or natural state. The nucleic acid, polynucleotide, or nucleotide sequences of the invention have been isolated, purified (or partially purified), by separation methods including, but not limited to, ion-exchange chromatography, molecular size exclusion chromatography, affinity chromatography, or by genetic engineering methods such as amplification, cloning, subcloning or chemical synthesis.

[0011] A homologous polynucleotide or polypeptide sequence, for the purposes of the present invention, encompasses a sequence having a percentage identity with the polynucleotide or polypeptide sequences, set forth herein, of between at least (or at least about) 20.00% to 99.99% (inclusive). The aforementioned range of percent identity is to be taken as including, and providing written description and support for, any fractional percentage, in intervals of 0.01%, between 20.00% and, up to, including 99.99%. These percentages are purely statistical and differences between two nucleic acid sequences can be distributed randomly and over the entire sequence length.

[0012] In various embodiments, homologous sequences can exhibit a percent identity of 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99 percent with the sequences of the instant invention. Typically, the percent identity is calculated with reference to the full length, native, and/or naturally occurring polypeptide or polynucleotide (*e.g.*, those polypeptides set forth in SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27 or those set forth in SEQ ID NOs:28-81)). The terms "identical" or percent "identity", in the context of two or more polynucleotide or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues that are the same, when compared and aligned for maximum correspondence over a comparison window, as measured using a sequence comparison algorithm or by manual alignment and visual inspection. Preferably, such a substitution is made in accordance with analoging principles set forth, *e.g.*, in co-pending U.S. Ser. No. 09/260,714 filed Mar. 1, 1999 and 09/226,775, filed January 6, 1999 and PCT application number PCT/US00/19774 each of which is hereby incorporated by reference in its entirety.

[0013] Both protein and nucleic acid sequence homologies may be evaluated using any of the variety of sequence comparison algorithms and programs known in the art. Such algorithms and programs include, but are by no means limited to, TBLASTN, BLASTP, FASTA, TFASTA, and CLUSTALW (Pearson and Lipman, 1988, *Proc. Natl. Acad. Sci. USA 85(8)*:2444-2448; Altschul *et al.*, 1990, *J. Mol. Biol. 215(3)*:403-410; Thompson *et al.*, 1994, *Nucleic Acids Res. 22(2)*:4673-4680; Higgins *et al.*, 1996, *Methods Enzymol. 266*:383-402; Altschul *et al.*, 1990, *J. Mol. Biol. 215(3)*:403-410; Altschul *et al.*, 1993, *Nature Genetics 3*:266-272). Sequence comparisons are, typically, conducted using default parameters provided by the vendor or using those parameters set forth in the above-identified references, which are hereby incorporated by reference in their entireties.

[0014] A "complementary" polynucleotide sequence, as used herein, generally refers to a sequence arising from the hydrogen bonding between a particular purine and a particular pyrimidine in double-stranded nucleic acid molecules (DNA-DNA, DNA-

RNA, or RNA-RNA). The major specific pairings are guanine with cytosine and adenine with thymine or uracil. A "complementary" polynucleotide sequence may also be referred to as an "antisense" polynucleotide sequence or an "antisense" sequence.

[0015] Sequence homology and sequence identity can also be determined by hybridization studies under high stringency, intermediate stringency, and/or low stringency. Various degrees of stringency of hybridization can be employed. The more severe the conditions, the greater the complementarity that is required for duplex formation. Severity of conditions can be controlled by temperature, probe concentration, probe length, ionic strength, time, and the like. Preferably, hybridization is conducted under low, intermediate, or high stringency conditions by techniques well known in the art, as described, for example, in Keller, G.H., M.M. Manak [1987] *DNA Probes*, Stockton Press, New York, NY, pp. 169-170.

[0016] For example, hybridization of immobilized DNA on Southern blots with ^{32}P-labeled gene-specific probes can be performed by standard methods (Maniatis *et al.* [1982] *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, New York). In general, hybridization and subsequent washes can be carried out under intermediate to high stringency conditions that allow for detection of target sequences with homology to the exemplified polynucleotide sequence. For double-stranded DNA gene probes, hybridization can be carried out overnight at 20-25° C below the melting temperature (T_m) of the DNA hybrid in 6X SSPE, 5X Denhardt's solution, 0.1% SDS, 0.1 mg/ml denatured DNA. The melting temperature is described by the following formula (Beltz *et al.* [1983] *Methods of Enzymology*, R. Wu, L. Grossman and K. Moldave [eds.] Academic Press, New York 100:266-285).

[0017] $Tm=81.5°C+16.6\ Log[Na^+]+0.41(\%G+C)-0.61(\%formamide)-600/length$ of duplex in base pairs.

[0018] Washes are typically carried out as follows:

(1) twice at room temperature for 15 minutes in 1X SSPE, 0.1% SDS (low stringency wash);

(2) once at T_m - 20°C for 15 minutes in 0.2X SSPE, 0.1% SDS (intermediate stringency wash).

[0019] For oligonucleotide probes, hybridization can be carried out overnight at 10-20°C below the melting temperature (T_m) of the hybrid in 6X SSPE, 5X Denhardt's solution, 0.1% SDS, 0.1 mg/ml denatured DNA. T_m for oligonucleotide probes can be determined by the following formula:

[0020] T_m (°C)=2(number T/A base pairs)+4(number G/C base pairs) (Suggs *et al.* [1981] *ICN-UCLA Symp. Dev. Biol. Using Purified Genes*, D.D. Brown [ed.], Academic Press, New York, 23:683-693).

[0021] Washes can be carried out as follows:

(1) twice at room temperature for 15 minutes 1X SSPE, 0.1% SDS (low stringency wash);

2) once at the hybridization temperature for 15 minutes in 1X SSPE, 0.1% SDS (intermediate stringency wash).

[0022] In general, salt and/or temperature can be altered to change stringency. With a labeled DNA fragment >70 or so bases in length, the following conditions can be used:

Low:	1 or 2X SSPE, room temperature
Low:	1 or 2X SSPE, 42°C
Intermediate:	0.2X or 1X SSPE, 65°C
High:	0.1X SSPE, 65°C.

[0023] By way of another non-limiting example, procedures using conditions of high stringency can also be performed as follows: Pre-hybridization of filters containing DNA is carried out for 8 h to overnight at 65°C in buffer composed of 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 µg/ml denatured salmon sperm DNA. Filters are hybridized for 48 h at 65°C, the preferred hybridization temperature, in pre-hybridization mixture containing 100 µg/ml denatured salmon sperm DNA and 5-20 x 10^6 cpm of ^{32}P-labeled probe. Alternatively, the hybridization step can be performed at 65°C in the presence of SSC buffer, 1X SSC

corresponding to 0.15M NaCl and 0.05 M Na citrate. Subsequently, filter washes can be done at 37°C for 1 h in a solution containing 2X SSC, 0.01% PVP, 0.01% Ficoll, and 0.01% BSA, followed by a wash in 0.1X SSC at 50°C for 45 min. Alternatively, filter washes can be performed in a solution containing 2X SSC and 0.1% SDS, or 0.5X SSC and 0.1% SDS, or 0.1X SSC and 0.1% SDS at 68°C for 15 minute intervals. Following the wash steps, the hybridized probes are detectable by autoradiography. Other conditions of high stringency which may be used are well known in the art and as cited in Sambrook *et al.*, 1989, Molecular Cloning, A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel *et al.*, 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are incorporated herein in their entirety.

[0024] Another non-limiting example of procedures using conditions of intermediate stringency are as follows: Filters containing DNA are pre-hybridized, and then hybridized at a temperature of 60°C in the presence of a 5X SSC buffer and labeled probe. Subsequently, filters washes are performed in a solution containing 2X SSC at 50°C and the hybridized probes are detectable by autoradiography. Other conditions of intermediate stringency which may be used are well known in the art and as cited in Sambrook *et al.*, 1989, Molecular Cloning, A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel *et al.*, 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are incorporated herein in their entirety.

[0025] Duplex formation and stability depend on substantial complementarity between the two strands of a hybrid and, as noted above, a certain degree of mismatch can be tolerated. Therefore, the probe sequences of the subject invention include mutations (both single and multiple), deletions, insertions of the described sequences, and combinations thereof, wherein said mutations, insertions and deletions permit formation of stable hybrids with the target polynucleotide of interest. Mutations, insertions and deletions can be produced in a given polynucleotide sequence in many ways, and these methods are known to an ordinarily skilled artisan. Other methods may become known in the future.

[0026] It is also well known in the art that restriction enzymes can be used to obtain functional fragments of the subject DNA sequences. For example, *Bal*31

exonuclease can be conveniently used for time-controlled limited digestion of DNA (commonly referred to as "erase-a-base" procedures). See, for example, Maniatis *et al.* [1982] *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, New York; Wei *et al.* [1983] *J. Biol. Chem.* 258:13006-13512.

[0027] The present invention further comprises fragments of the polynucleotide sequences of the instant invention. Representative fragments of the polynucleotide sequences according to the invention will be understood to mean any nucleotide fragment having at least 8 successive nucleotides, preferably at least 12 successive nucleotides, and still more preferably at least 15 or at least 20 successive nucleotides of the sequence from which it is derived. The upper limit for such fragments is the total number of polynucleotides found in the full length sequence (or, in certain embodiments, of the full length open reading frame (ORF) identified herein).

[0028] In some embodiments, the subject invention includes those fragments capable of hybridizing under various conditions of stringency conditions (*e.g.*, high or intermediate or low stringency) with a nucleotide sequence according to the invention; fragments that hybridize with a nucleotide sequence of the subject invention can be, optionally, labeled as set forth below.

[0029] Other embodiments provide for nucleic acid fragments corresponding to nucleotide sequences comprising full, or partial, open reading frames (ORF sequences). Also within the scope of the invention are those polynucleotide fragments encoding polypeptides reactive with antibodies found in the serum of individuals infected with *P. falciparum*. Fragments according to the subject invention can be obtained, for example, by specific amplification (*e.g.*, PCR amplification), digestion with restriction enzymes, of nucleotide sequences according to the invention. Such methodologies are well-known in the art and are taught, for example, by Sambrook *et al.*, 1989. Nucleic acid fragments according to the invention can also be obtained by chemical synthesis according to methods well known to persons skilled in the art.

[0030] The subject invention also provides nucleic acid based methods for the identification of the presence of an organism in a sample. In these varied embodiments, the invention provides for the detection of nucleic acids in a sample comprising contacting a sample with a nucleic acid (polynucleotide) of the subject invention (such as

an RNA, mRNA, DNA, cDNA, or other nucleic acid). In a preferred embodiment, the polynucleotide is a probe that is, optionally, labeled and used in the detection system. Many methods for detection of nucleic acids exist and any suitable method for detection is encompassed by the instant invention. Typical assay formats utilizing nucleic acid hybridization includes, and are not limited to, 1) nuclear run-on assay, 2) slot blot assay, 3) northern blot assay (Alwine, *et al.* Proc. Natl. Acad. Sci. 74:5350), 4) magnetic particle separation, 5) nucleic Acid or DNA chips, 6) reverse Northern blot assay, 7) dot blot assay, 8) in situ hybridization, 9) RNase protection assay (Melton, *et al.* Nuc. Acids Res. 12:7035 and as described in the 1998 catalog of Ambion, Inc., Austin, Tex.), 10) ligase chain reaction, 11) polymerase chain reaction (PCR), 12) reverse transcriptase (RT)-PCR (Berchtold, *et al.* Nuc. Acids. Res. 17:453), 13) differential display RT-PCR (DDRT-PCR) or other suitable combinations of techniques and assays. Labels suitable for use in these detection methodologies include, and are not limited to 1) radioactive labels, 2) enzyme labels, 3) chemiluminescent labels, 4) fluorescent labels, 5) magnetic labels, or other suitable labels, including those set forth below. These methodologies and labels are well known in the art and widely available to the skilled artisan. Likewise, methods of incorporating labels into the nucleic acids are also well known to the skilled artisan.

[0031] Thus, the subject invention also provides detection probes (*e.g.*, fragments of the disclosed polynucleotide sequences) for hybridization with a target sequence or the amplicon generated from the target sequence. Such a detection probe will advantageously have as sequence a sequence of at least 8, 9, 10, 11, 12, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 nucleotides. Labeled probes or primers are labeled with a radioactive compound or with another type of label as set forth above. Alternatively, non-labeled nucleotide sequences may be used directly as probes or primers; however, the sequences are generally labeled with a radioactive element (^{32}P, ^{35}S, ^{3}H, ^{125}I) or with a molecule such as biotin, acetylaminofluorene, digoxigenin, 5-bromo-deoxyuridine, or fluorescein to provide probes that can be used in numerous applications.

[0032] The polynucleotide sequences according to the invention may also be used in analytical systems, such as DNA chips. DNA chips and their uses are well known in the art and (see for example, U.S. Patent Nos. 5,561,071; 5,753,439; 6,214,545; *Schena et al.*, BioEssays, 1996, 18:427-431; *Bianchi et al.*, Clin. Diagn. Virol., 1997, 8:199-208;

each of which is hereby incorporated by reference in their entireties) and/or are provided by commercial vendors such as Affymetrix, Inc. (Santa Clara, CA). In addition, the nucleic acid sequences of the subject invention can be used as molecular weight markers in nucleic acid analysis procedures.

[0033] The subject invention also provides for modified nucleotide sequences. Modified nucleic acid sequences will be understood to mean any nucleotide sequence that has been modified, according to techniques well known to persons skilled in the art, and exhibiting modifications in relation to the native, naturally occurring nucleotide sequences. One non-limiting example of a "modified" nucleotide sequences includes mutations in regulatory and/or promoter sequences of a polynucleotide sequence that result in a modification of the level of expression of the polypeptide. A "modified" nucleotide sequence will also be understood to mean any nucleotide sequence encoding a "modified" polypeptide as defined below.

[0034] Another aspect of the invention provides vectors for the cloning and/or the expression of a polynucleotide sequence taught herein. Vectors of this invention, including vaccine vectors, can also comprise elements necessary to allow the expression and/or the secretion of the said nucleotide sequences in a given host cell. The vector can contain a promoter, signals for initiation and for termination of translation, as well as appropriate regions for regulation of transcription. In certain embodiments, the vectors can be stably maintained in the host cell and can, optionally, contain signal sequences directing the secretion of translated protein. These different elements are chosen according to the host cell used. Vectors can integrate into the host genome or, optionally, be autonomously-replicating vectors.

[0035] The subject invention also provides for the expression of a polypeptide, peptide, derivative, or variant encoded by a polynucleotide sequence disclosed herein comprising the culture of an organism transformed with a polynucleotide of the subject invention under conditions that allow for the expression of the polypeptide, peptide, derivative, or analog and, optionally, recovering the expressed polypeptide, peptide, derivative, or analog.

[0036] The disclosed polynucleotide sequences can also be regulated by a second nucleic acid sequence so that the protein or peptide is expressed in a host transformed

with the recombinant DNA molecule. For example, expression of a protein or peptide may be controlled by any promoter/enhancer element known in the art. Promoters which may be used to control expression include, but are not limited to, the CMV-IE promoter, the SV40 early promoter region (Bernoist and Chambon, 1981, Nature 290:304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto, *et al.*, 1980, Cell 22:787-797), the herpes simplex thymidine kinase promoter (Wagner *et al.*, 1981, Proc. Natl. Acad. Sci. U.S.A. 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster *et al.*, 1982, Nature 296:39-42); prokaryotic vectors containing promoters such as the β-lactamase promoter (Villa-Kamaroff, *et al.*, 1978, Proc. Natl. Acad. Sci. U.S.A. 75:3727-3731), or the *tac* promoter (DeBoer, *et al.*, 1983, Proc. Natl. Acad. Sci. U.S.A. 80:21-25); see also "Useful proteins from recombinant bacteria" in Scientific American, 1980, 242:74-94; plant expression vectors comprising the nopaline synthetase promoter region (Herrera-Estrella *et al.*, 1983, Nature 303:209-213) or the cauliflower mosaic virus 35S RNA promoter (Gardner, *et al.*, 1981, Nucl. Acids Res. 9:2871), and the promoter of the photosynthetic enzyme ribulose biphosphate carboxylase (Herrera-Estrella *et al.*, 1984, Nature 310:115-120); promoter elements from yeast or fungi such as the Gal 4 promoter, the ADC (alcohol dehydrogenase) promoter, PGK (phosphoglycerol kinase) promoter, and/or the alkaline phosphatase promoter.

[0037] The vectors according to the invention are, for example, vectors of plasmid or viral origin. In a specific embodiment, a vector is used that comprises a promoter operably linked to a protein or peptide-encoding nucleic acid sequence contained within the disclosed polynucleotide sequences, one or more origins of replication, and, optionally, one or more selectable markers (*e.g.*, an antibiotic resistance gene). Expression vectors comprise regulatory sequences that control gene expression, including gene expression in a desired host cell. Exemplary vectors for the expression of the polypeptides of the invention include the pET-type plasmid vectors (Promega) or pBAD plasmid vectors (Invitrogen) or those provided in the examples below. Furthermore, the vectors according to the invention are useful for transforming host cells so as to clone or express the polynucleotide sequences of the invention.

[0038] The invention also encompasses the host cells transformed by a vector according to the invention. These cells may be obtained by introducing into host cells a nucleotide sequence inserted into a vector as defined above, and then culturing the said

cells under conditions allowing the replication and/or the expression of the polynucleotide sequences of the subject invention.

[0039] The host cell may be chosen from eukaryotic or prokaryotic systems, such as for example bacterial cells, (Gram negative or Gram positive), yeast cells (for example, *Saccharomyces cereviseae* or *Pichia pastoris*), animal cells (such as Chinese hamster ovary (CHO) cells), plant cells, and/or insect cells using baculovirus vectors. In some embodiments, the host cells for expression of the polypeptides include, and are not limited to, those taught in U.S. Patent Nos. 6,319,691, 6,277,375, 5,643,570, or 5,565,335, each of which is incorporated by reference in its entirety, including all references cited within each respective patent.

[0040] Furthermore, a host cell strain may be chosen which modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Expression from certain promoters can be elevated in the presence of certain inducers; thus, expression of the genetically engineered polypeptide may be controlled. Furthermore, different host cells have characteristic and specific mechanisms for the translational and post-translational processing and modification (*e.g.*, glycosylation, phosphorylation) of proteins. Appropriate cell lines or host systems can be chosen to ensure the desired modification and processing of the foreign protein expressed. For example, expression in a bacterial system can be used to produce an unglycosylated core protein product. Expression in yeast will produce a glycosylated product. Expression in mammalian cells can be used to ensure "native" glycosylation of a heterologous protein. Furthermore, different vector/host expression systems may effect processing reactions to different extents.

[0041] The subject invention also concerns novel compositions that can be employed to elicit an immune response or a protective immune response. In this aspect of the invention, an amount of a composition comprising recombinant DNA or mRNA encoding an polynucleotide of the subject invention sufficient to elicit an immune response or protective immune response is administered to an individual. Signal sequences may be deleted from the nucleic acid encoding an antigen of interest and the individual may be monitored for the induction of an immune response according to methods known in the art. A "protective immune response" or "therapeutic immune response" refers to a CTL (or $CD8^+$ T cell) and/or an HTL (or $CD4^+$ T cell) response to

an antigen that, in some way, prevents or at least partially arrests disease symptoms, side effects or progression. The immune response may also include an antibody response that has been facilitated by the stimulation of helper T cells.

[0042] In another embodiment, the subject invention further comprises the administration of polynucleotide vaccines in conjunction with a polypeptide antigen, or composition thereof, of the invention. In a preferred embodiment, the antigen is the polypeptide that is encoded by the polynucleotide administered as the polynucleotide vaccine. As a particularly preferred embodiment, the polypeptide antigen is administered as a booster subsequent to the initial administration of the polynucleotide vaccine.

[0043] A further embodiment of the subject invention provides for the induction of an immune response to the novel *Plasmodium falciparum* antigens disclosed herein (see, for example, the antigens and peptides set forth in the Tables and Sequence Listing attached hereto) using a "prime-boost" vaccination regimen known to those skilled in the art. In this aspect of the invention, a DNA vaccine is administered to an individual in an amount sufficient to "prime" the immune response of the individual, provided that the DNA vaccine comprises nucleic acids encoding the antigens, multi-epitope constructs, and/or peptide antigens set forth herein. The immune response of the individual is then "boosted" via the administration of: 1) one or a combination of: a peptide, polypeptide, and/or full length polypeptide antigen (*e.g.*, SEQ ID NOs: 1-27) of the subject invention (optionally in conjunction with a immunostimulatory molecule and/or an adjuvant); or 2) a viral vector that contains nucleic acid encoding one, or more, of the same or, optionally, different, antigens, multi-epitope constructs, and/or peptide antigens set forth in the Tables or Sequence Listing of the subject application. In some alternative embodiments of the invention, a gene encoding an immunostimulatory molecule may be incorporated into the viral vector used to "boost the immune response of the individual. Exemplary immunostimulatory molecules include, and are not limited to, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-15, Il-16, Il-18, IL-23, IL-24, erythropoietin, G-CSF, M-CSF, platelet derived growth factor (PDGF), MSF, FLT-3 ligand, EGF, fibroblast growth factor (FGF; *e.g.*, aFGF (FGF-1), bFGF (FGF-2), FGF-3, FGF-4, FGF-5, FGF-6, or FGF-7), insulin-like growth factors (*e.g.*, IGF-1, IGF-2); vascular endothelial growth factor (VEGF); interferons (*e.g.*, IFN-γ, IFN-α, IFN-β); leukemia inhibitory factor (LIF); ciliary neurotrophic factor (CNTF); oncostatin M; stem cell factor

(SCF); transforming growth factors (*e.g.*, TGF-α, TGF-β1, TGF-β1, TGF-β1), or chemokines (such as, but not limited to, BCA-1/BLC-1, BRAK/Kec, CXCL16, CXCR3, ENA-78/LIX, Eotaxin-1, Eotaxin-2/MPIF-2, Exodus-2/SLC, Fractalkine/Neurotactin, GROalpha/MGSA, HCC-1, I-TAC, Lymphotactin/ATAC/SCM, MCP-1/MCAF, MCP-3, MCP-4, MDC/STCP-1, ABCD-1, MIP-1α, MIP-1β, MIP-2α/GROβ, MIP-3α/Exodus/LARC, MIP-3β/Exodus-3/ELC, MIP-4/PARC/DC-CK1, PF-4, RANTES, SDF1α, TARC, or TECK). Genes encoding these immunostimulatory molecules are known to those skilled in the art and coding sequences may be obtained from a variety of sources, including various patents databases, publicly available databases (such as the nucleic acid and protein databases found at the National Library of Medicine or the European Molecular Biology Laboratory), the scientific literature, or scientific literature cited in catalogs produced by companies such as Genzyme, Inc., R&D Systems, Inc, or InvivoGen, Inc. [see, for example, the 1995 Cytokine Research Products catalog, Genzyme Diagnostics, Genzyme Corporation, Cambridge MA; 2002 or 1995 Catalog of R&D Systems, Inc (Minneapolis, MN); or 2002 Catalog of InvivoGen, Inc (San Diego, CA) each of which is incorporated by reference in its entirety, including all references cited therein].

[0044] Methods of introducing DNA vaccines into individuals are well-known to the skilled artisan. For example, DNA can be injected into skeletal muscle or other somatic tissues (e.g., intramuscular injection). Cationic liposomes or biolistic devices, such as a gene gun, can be used to deliver DNA vaccines. Alternatively, iontophoresis and other means for transdermal transmission can be used for the introduction of DNA vaccines into an individual.

[0045] Viral vectors for use in the subject invention can have a portion of the viral genome deleted to introduce new genes without destroying infectivity of the virus. The viral vector of the present invention is, typically, a non-pathogenic virus. At the option of the practitioner, the viral vector can be selected so as to infect a specific cell type, such as professional antigen presenting cells (*e.g.*, macrophage or dendritic cells). Alternatively, a viral vector can be selected that is able to infect any cell in the individual. Exemplary viral vectors suitable for use in the present invention include, but are not limited to poxvirus such as vaccinia virus, avipox virus, fowlpox virus, a highly attenuated vaccinia

virus (such as Ankara or MVA [Modified Vaccinia Ankara]), retrovirus, adenovirus, baculovirus and the like. In a preferred embodiment, the viral vector is Ankara or MVA.

[0046] General strategies for construction of vaccinia virus expression vectors are known in the art (see, for example, Smith and Moss Bio Techniques Nov/Dec, 306-312, 1984; U.S. Patent No. 4,738,846 (hereby incorporated by reference in its entirety). Sutter and Moss (Proc. Nat'l. Acad. Sci U.S.A. 89:10847-10851, 1992) and Sutter et al. (Vaccine, 12(11):1032-40, 1994) disclose the construction and use as a vector, a non-replicating recombinant Ankara virus (MVA) which can be used as a viral vector in the present invention. Other versions of the Modified Vaccinia Ankara strain can also be used in the practice of the subject invention (such as the MVA-BN strain produced by Bavarian Nordic S/A (Copenhagen, Denmark).

[0047] Compositions comprising the subject polynucleotides can include appropriate nucleic acid vaccine vectors (plasmids), which are commercially available (*e.g.*, Vical, San Diego, CA) or other nucleic acid vectors (plasmids), which are also commercially available (*e.g.*, Valenti, Burlingame, CA). Alternatively, compositions comprising viral vectors and polynucleotides according to the subject invention are provided by the subject invention. In addition, the compositions can include a pharmaceutically acceptable carrier, *e.g.*, saline. The pharmaceutically acceptable carriers are well known in the art and also are commercially available. For example, such acceptable carriers are described in E.W. Martin's *Remington's Pharmaceutical Science*, Mack Publishing Company, Easton, PA.

[0048] The subject invention also provides one or more isolated polypeptides comprising:

a) a polypeptide encoded by a polynucleotide sequence according to embodiment A(a) (set forth above);

b) a variant polypeptide encoded by a polynucleotide sequence having at least about 20% to 99.99% identity to a polynucleotide according to embodiment A(a) (as set forth above);

c) a fragment of a polypeptide or a variant polypeptide, wherein said fragment or variant has substantially the same serologic reactivity or substantially the same T-cell reactivity as the native polypeptide (*e.g.*, those polypeptides set

forth in SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27 and Table 2, 3, 4, 5 or 6);

d) a polypeptide sequence provided in Table 2, 3, 4, 5 or 6 or selected from the group consisting of SEQ ID NO: NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27;

e) a variant polypeptide having at least about 20% to 99.99% identity to a polypeptide provided in Table 2, 3, 4, 5 or 6 or selected from the group consisting of SEQ ID NO: NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27;

f) a polypeptide (epitope) set forth in Table 2, 3, 4, 5 or 6; or

g) a multi-epitope construct: 1) comprising at least one epitope set forth in Table 2, 3, 4, 5 or 6; 2) comprising a polypeptide selected from the group consisting of SEQ ID NO: NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27 and at least one epitope set forth in Tables 2, 3, 4, 5 or 6; or 3) comprising and at least one epitope set forth in Tables 2, 3, 4, 5 or 6 and one or more polypeptide selected from the group consisting of SEQ ID NO: NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27.

[0049] The term "peptide" may be used interchangeably with "oligopeptide" or "polypeptide" or "epitope" in the present specification to designate a series of residues, typically L-amino acids, connected one to the other, typically by peptide bonds between the α-amino and carboxyl groups of adjacent amino acids. The preferred CTL (or $CD8^+$ T cell)-inducing peptides of the invention are 13 residues or less in length and usually consist of between about 8 and about 11 residues (*e.g.*, 8, 9, 10 or 11 residues), preferably 9 or 10 residues. The preferred HTL (or $CD4^+$ T cell)-inducing peptides are less than about 50 residues in length and usually consist of between about 6 and about 30 residues, more usually between about 12 and 25 (*e.g.*, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or 25), and often between about 15 and 20 residues (*e.g.*, 15, 16, 17, 18, 19 or 20).

[0050] According to the subject invention, a "fragment" is a polypeptide of at least 3 consecutive, preferably 4 consecutive, and even more preferably 5 consecutive amino acids. In some embodiments, the polypeptide fragments are reactive with antibodies found in the serum of an individual. In other embodiments, a fragment is

an "epitope" as described *supra*. In the context of the instant invention, the terms polypeptide, peptide and protein can be used interchangeably; however, it should be understood that the invention does not relate to the polypeptides in natural form, that is to say that they are not in their natural environment but that the polypeptides may have been isolated or obtained by purification from natural sources, obtained from host cells prepared by genetic manipulation (*e.g.*, the polypeptides, or fragments thereof, are recombinantly produced by host cells, or by chemical synthesis). Polypeptides according to the instant invention may also contain non-natural amino acids, as will be described below.

[0051] A "variant" or "modified" polypeptide (or polypeptide variant) is to be understood to designate polypeptides exhibiting, in relation to the natural polypeptide, certain modifications. These modifications can include a deletion, addition, or substitution of at least one amino acid, a truncation, an extension, a chimeric fusion, a mutation, or polypeptides exhibiting post-translational modifications. Among the homologous polypeptides, those whose amino acid sequences exhibit between at least (or at least about) 20.00% to 99.99% (inclusive) identity to the full length, native, or naturally occurring polypeptide are another aspect of the invention. The aforementioned range of percent identity is to be taken as including, and providing written description and support for, any fractional percentage, in intervals of 0.01%, between 20.00% and, up to, including 99.99%. These percentages are purely statistical and differences between two polypeptide sequences can be distributed randomly and over the entire sequence length.

[0052] Variant peptides (epitopes) can also be created by altering the presence or absence of particular residues in these primary anchor positions. Such analogs are used to modulate the binding affinity of a peptide comprising a particular motif or supermotif. The term "motif" refers to the pattern of residues in a peptide of defined length, usually a peptide of from about 8 to about 13 amino acids for a class I HLA motif (*e.g.*, 8, 9, 10, 11, 12 or 13 aa) and from about 6 to about 25 amino acids for a class II HLA motif (*e.g.*, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or 25 amino acids), which is recognized by a particular HLA molecule. Peptide motifs are typically different for each protein encoded by each human HLA allele and differ in the pattern of the primary and secondary anchor residues. Optionally, variant peptides or polypeptides can also comprise one or more heterologous polypeptide sequences (*e.g.*, tags that facilitate

purification of the polypeptides of the invention (see, for example, U.S. Patent No. 6,342,362, hereby incorporated by reference in its entirety; Altendorf *et al.* [1999-WWW, 2000] "Structure and Function of the F_o Complex of the ATP Synthase from *Escherichia Coli*," *J. of Experimental* Biology 203:19-28, The Co. of Biologists, Ltd., G.B.; Baneyx [1999] "Recombinant Protein Expression in *Escherichia coli*," Biotechnology 10:411-21, Elsevier Science Ltd.; Eihauer *et al.* [2001] "The FLAG™ Peptide, a Versatile Fusion Tag for the Purification of Recombinant Proteins," *J. Biochem Biophys Methods* 49:455-65; Jones *et al.* [1995] *J. Chromatography* 707:3-22; Jones *et al.* [1995] "Current Trends in Molecular Recognition and Bioseparation," *J. of Chromatography A.* 707:3-22, Elsevier Science B.V.; Margolin [2000] "Green Fluorescent Protein as a Reporter for Macromolecular Localization in Bacterial Cells," *Methods* 20:62-72, Academic Press; Puig *et al.* [2001] "The Tandem Affinity Purification (TAP) Method: A General Procedure of Protein Complex Purification," *Methods* 24:218-29, Academic Press; Sassenfeld [1990] "Engineering Proteins for Purification," TibTech 8:88-93; Sheibani [1999] "Prokaryotic Gene Fusion Expression Systems and Their Use in Structural and Functional Studies of Proteins," *Prep. Biochem. & Biotechnol.* 29(1):77-90, Marcel Dekker, Inc.; Skerra *et al.* [1999] "Applications of a Peptide Ligand for Streptavidin: the *Strep*-tag", *Biomolecular Engineering* 16:79-86, Elsevier Science, B.V.; Smith [1998] "Cookbook for Eukaryotic Protein Expression: Yeast, Insect, and Plant Expression Systems," *The* Scientist 12(22):20; Smyth *et al.* [2000] "Eukaryotic Expression and Purification of Recombinant Extracellular Matrix Proteins Carrying the Strep II Tag", *Methods in Molecular Biology*, 139:49-57; Unger [1997] "Show Me the Money: Prokaryotic Expression Vectors and Purification Systems," *The Scientist* 11(17):20, each of which is hereby incorporated by reference in their entireties), or commercially available tags from vendors such as such as STRATAGENE (La Jolla, CA), NOVAGEN (Madison, WI), QIAGEN, Inc., (Valencia, CA), or InVitrogen (San Diego, CA).

[0053] Variant polypeptides can, alternatively, have 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99 percent identity with the polypeptide sequences of the instant invention. In a preferred embodiment, a variant or modified polypeptide exhibits approximately 85%, 86%, 87%,

88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to a natural polypeptic of the invention. Typically, the percent identity is calculated with reference to the full length, native, and/or naturally occurring polypeptide (*e.g.*, those polypeptides set forth in SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, or 27).

[0054] The nomenclature used to describe peptide compounds follows the conventional practice wherein the amino group is presented to the left (the N-terminus) and the carboxyl group to the right (the C-terminus) of each amino acid residue. When amino acid residue positions are referred to in an epitope, they are numbered in an amino to carboxyl direction with position one being the position closest to the amino terminal end of the epitope, or the peptide or protein of which it may be a part. In the formulae representing selected specific embodiments of the present invention, the amino- and carboxyl-terminal groups, although not specifically shown, are in the form they would assume at physiologic pH values, unless otherwise specified. In the amino acid structure formulae, each residue is generally represented by standard three-letter or single-letter designations (*e.g.*, as set forth *infra)*. By way of example, amino acid substitutions can be carried out without resulting in a substantial modification of the biological activity of the corresponding modified polypeptides; for example, the replacement of leucine with valine or isoleucine, of aspartic acid with glutamic acid, of glutamine with asparagine, of arginine with lysine, and the like, the reverse substitutions can be performed without substantial modification of the biological activity of the polypeptides.

[0055] The L-form of an amino acid residue is represented by a capital single letter or a capital first letter of a three-letter symbol, and the D-form, for those amino acids having D-forms, is represented by a lower case single letter or a lower case three letter symbol. Glycine has no asymmetric carbon atom and is simply referred to as "Gly" or G. Symbols for the amino acids are as follows: (Single Letter Symbol; Three Letter Symbol Amino Acid) A; Ala; Alanine: C; Cys; Cysteine: D; Asp; Aspartic Acid: E; Glu; Glutamic Acid: F; Phe; Phenylalanine: G; Gly; Glycine: H; His; Histidine: I; Ile; Isoleucine: K; Lys; Lysine: L; Leu; Leucine: M; Met; Methionine: N; Asn; Asparagine: P; Pro; Proline: Q; Gln; Glutamine: R; Arg; Arginine: S; Ser; Serine: T; Thr; Threonine: V; Val; Valine: W; Trp; Tryptophan: Y; Tyr; Tyrosine.

[0056] Amino acid "chemical characteristics" are defined as: Aromatic (F, W, Y); Aliphatic-hydrophobic (L, I, V, M); Small polar (S, T, C); Large polar (Q, N); Acidic (D, E); Basic (R, H, K); Non-polar: Proline; Alanine; and Glycine.

[0057] In order to extend the life of the polypeptides according to the invention, it may be advantageous to use non-natural amino acids, for example in the D-form, or alternatively amino acid analogs, for example sulfur-containing forms of amino acids in the production of "variant polypeptides". Alternative means for increasing the life of polypeptides can also be used in the practice of the instant invention. For example, polypeptides of the invention, and fragments thereof, can be recombinantly modified to include elements that increase the plasma, or serum half-life of the polypeptides of the invention. These elements include, and are not limited to, antibody constant regions (see for example, U.S. Patent No. 5,565,335, hereby incorporated by reference in its entirety, including all references cited therein), or other elements such as those disclosed in U.S. Patent Nos. 6,319,691, 6,277,375, or 5,643,570, each of which is incorporated by reference in its entirety, including all references cited within each respective patent. Alternatively, the polynucleotides and genes of the instant invention can be recombinantly fused to elements, well known to the skilled artisan, that are useful in the preparation of immunogenic constructs for the purposes of vaccine formulation.

[0058] The subject invention also provides biologically active fragments (epitopes) of a polypeptide according to the invention and includes those peptides capable of eliciting an immune response directed against *P. falciparum*, said immune response providing components (B-cells, antibodies, and/or or components of the cellular immune response (*e.g.*, helper, cytotoxic, and/or suppressor T-cells)) reactive with the biologically active fragment of a polypeptide; the intact, full length, unmodified polypeptide disclosed herein; or both the biologically active fragment of a polypeptide and the intact, full length, unmodified polypeptides disclosed herein.

[0059] Fragments, as described herein, can be obtained by cleaving the polypeptides of the invention with a proteolytic enzyme (such as trypsin, chymotrypsin, or collagenase) or with a chemical reagent, such as cyanogen bromide (CNBr). Alternatively, polypeptide fragments can be generated in a highly acidic environment, for example at pH 2.5. Such polypeptide fragments may be equally well prepared by chemical synthesis or using hosts transformed with an expression vector according to the

invention. The transformed host cells contain a nucleic acid, allowing the expression of these fragments, under the control of appropriate elements for regulation and/or expression of the polypeptide fragments.

[0060] In one embodiment, the subject invention provides methods for eliciting an immune response in an individual comprising the administration of compositions comprising polypeptides according to the subject invention to an individual in amounts sufficient to induce an immune response in the individual. In some embodiments, a "protective" or "therapeutic immune response" is induced in the individual. A "protective immune response" or "therapeutic immune response" refers to a CTL (or $CD8^+$ T cell) and/or an HTL (or $CD4^+$ T cell), and/or an antibody response to an antigen derived from an infectious agent or a tumor antigen, which in some way prevents or at least partially arrests disease symptoms, side effects or progression. The protective immune response may also include an antibody response that has been facilitated by the stimulation of helper T cells (or $CD4^+$ T cells). Additional methods of inducing an immune response in an individual are taught in U.S. Patent No. 6,419,931, hereby incorporated by reference in its entirety. The term CTL can be used interchangeably with $CD8^+$ T-cell(s) and the term HTL can be used interchangeably with $CD4^+$ T-cell(s) throughout the subject application.

[0061] The term "individual" includes mammals which include, and are not limited to, apes, chimpanzees, orangutans, humans, monkeys or domesticated animals (pets) such as dogs, cats, guinea pigs, hamsters, Vietnamese pot-bellied pigs, rabbits, ferrets, cows, horses, goats and sheep. In a preferred embodiment, the methods of inducing an immune response contemplated herein are practiced on humans.

[0062] Another embodiment of the subject invention provides methods of inducing an immune response in an individual comprising the administration of a composition comprising polypeptides encoded by the polynucleotides of the subject invention in amounts sufficient to induce an immune response. In some embodiments of the invention, the immune response provides protective immunity. The composition administered to the individual may, optionally, contain an adjuvant and may be delivered in any manner known in the art for the delivery of immunogen to a subject. Compositions may also be formulated in any carriers, including for example, pharmaceutically acceptable carriers such as those described in E.W. Martin's

Remington's Pharmaceutical Science, Mack Publishing Company, Easton, PA. In a preferred embodiment, compositions may be formulated in incomplete Freund's adjuvant.

[0063] In various embodiments, the subject invention provides for diagnostic assays based upon Western blot formats or standard immunoassays known to the skilled artisan. For example, antibody-based assays such as enzyme linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), lateral flow assays, immunochromatographic strip assays, automated flow assays, and assays utilizing antibody-containing biosensors may be employed for the detection of the polypeptides, and fragments thereof, provided by the subject invention. The assays and methods for conducting the assays are well-known in the art and the methods may test biological samples qualitatively (presence or absence of polypeptide) or quantitatively (comparison of a sample against a standard curve prepared using a polypeptide of the subject invention) for the presence of one or more polypeptide of the subject invention. Thus, the subject invention provides a method of detecting a *P. falciparum* polypeptide, or fragment thereof, comprising contacting a sample with an antibody that specifically binds to a polypeptide, or fragment thereof, comprising SEQ ID NOs: 1-26, or 27 and detecting the presence of an antibody-antigen complex.

[0064] The antibody-based assays can be considered to be of four types: direct binding assays, sandwich assays, competition assays, and displacement assays. In a direct binding assay, either the antibody or antigen is labeled, and there is a means of measuring the number of complexes formed. In a sandwich assay, the formation of a complex of at least three components (*e.g.*, antibody-antigen-antibody) is measured. In a competition assay, labeled antigen and unlabelled antigen compete for binding to the antibody, and either the bound or the free component is measured. In a displacement assay, the labeled antigen is pre-bound to the antibody, and a change in signal is measured as the unlabelled antigen displaces the bound, labeled antigen from the receptor.

[0065] Lateral flow assays can be conducted according to the teachings of U.S. Patent No. 5,712,170 and the references cited therein. U.S. Patent No. 5,712,170 and the references cited therein are hereby incorporated by reference in their entireties. Displacement assays and flow immunosensors useful for carrying out displacement assays are described in: (1) Kusterbeck *et al.*, "Antibody-Based Biosensor for Continuous Monitoring", in Biosensor Technology, R. P. Buck *et al.*, eds., Marcel Dekker, N.Y. pp.

345-350 (1990); Kusterbeck *et al.*, "A Continuous Flow Immunoassay for Rapid and Sensitive Detection of Small Molecules", Journal of Immunological Methods, vol. 135, pp. 191-197 (1990); Ligler *et al.*, "Drug Detection Using the Flow Immunosensor", in Biosensor Design and Application, J. Findley *et al.*, eds., American Chemical Society Press, pp. 73-80 (1992); and Ogert *et al.*, "Detection of Cocaine Using the Flow Immunosensor", Analytical Letters, vol. 25, pp. 1999-2019 (1992), all of which are incorporated herein by reference in their entireties. Displacement assays and flow immunosensors are also described in U.S. Patent No. 5,183,740, which is also incorporated herein by reference in its entirety. The displacement immunoassay, unlike most of the competitive immunoassays used to detect small molecules, can generate a positive signal with increasing antigen concentration. One aspect of the invention allows for the exclusion of Western blots as a diagnostic assay, particularly where the Western blot is a screen of whole cell lysates of *P. falciparum*, or related organisms, against immune serum of infected individuals. In another aspect of the invention, peptide, or polypeptide, based diagnostic assays utilize *P. falciparum* peptides or polypeptides that have been produce either by chemical peptide synthesis or by recombinant methodologies that utilize non-plasmodium host cells for the production of peptides or polypeptides.

[0066] Another aspect of the invention provides for the use of peptides, polypeptides, and multi-epitope constructs in assays such as those taught in U.S. Patent No. 5,635,363, which is hereby incorporated by reference in its entirety. Briefly, peptides, polypeptides, and multi-epitope constructs of the subject invention can be used to form stable multimeric complexes that comprise prepared major histocompatibility complex (MHC) protein subunits having a substantially homogeneous bound peptide population. The multimeric MHC-antigen complex forms a stable structure with T cells recognizing the complex through their antigen receptor, thereby allowing for the labeling, identification and separation of specific T cells. The multimeric binding complex has the formula $(\alpha\text{-}\beta\text{-}P)_n$, where $n \geq 2$, usually $n \geq 4$, and usually $n \leq 10$; α is an α chain of a class I or class II MHC protein. β is a β chain, (the β chain of a class II MHC protein or β_2 microglobulin for a MHC class I protein; and P is a peptide antigen. The multimeric complex stably binds through non-covalent interactions to a T cell receptor having the appropriate antigenic specificity. The MHC proteins may be from any individual. Of particular interest are the human HLA proteins. Included in the HLA proteins are the

class II subunits HLA-DPα, HLA-DPβ, HLA-DQα, HLA-DQβ, HLA-DRα and HLA-DRβ, and the class I proteins HLA-A, HLA-B, HLA-C, and β_2 -microglobulin. In a preferred embodiment, the MHC protein subunits are a soluble form of the normally membrane-bound protein. The soluble form is derived from the native form by deletion of the transmembrane domain. Conveniently, the protein is truncated, removing both the cytoplasmic and transmembrane domains. The protein may be truncated by proteolytic cleavage, or by expressing a genetically engineered truncated form. For class I proteins, the soluble form will include the α1, α2 and α3 domain. Not more than about 10, usually not more than about 5, preferably none of the amino acids of the transmembrane domain will be included. The deletion may extend as much as about 10 amino acids into the α3 domain, preferably none of the amino acids of the α3 domain will be deleted. The deletion will be such that it does not interfere with the ability of the α3 domain to fold into a disulfide bonded structure. The class I β chain, β_2-microglobulin, lacks a transmembrane domain in its native form, and need not be truncated. Generally, no Class II subunits will be used in conjunction with Class I subunits. Soluble class II subunits will include the α1 and α2 domains for the α subunit, and the β1 and β2 domains for the β subunit. Not more than about 10, usually not more than about 5, preferably none of the amino acids of the transmembrane domain will be included. The deletion may extend as much as about 10 amino acids into the α2 or β2 domain, preferably none of the amino acids of the β2 or β2 domain will be deleted. The deletion will be such that it does not interfere with the ability of the α2 or β2 domain to fold into a disulfide bonded structure.

[0067] The monomeric complex (α-β-P) (monomer) is multimerized. The resulting multimer will be stable over long periods of time. Usually not more than about 10% of the multimer will be dissociated after storage at 4° C for about one day, more usually after about one week. Preferably, the multimer will be formed by binding the monomers to a multivalent entity through specific attachment sites on the α or β subunit, as described below in detail. The multimer may also be formed by chemical cross-linking of the monomers. A number of reagents capable of cross-linking proteins are known in the art, illustrative entities include: azidobenzoyl hydrazide, N-[4-(p-azidosalicylamino)butyl]-3'-[2'-pyridyldithio]propionamide), bis-sulfosuccinimidyl suberate, dimethyladipimidate, disuccinimidyltartrate, N-.gamma.-maleimidobutyryloxysuccinimide ester, N-hydroxy sulfosuccinimidyl-4-azidobenzoate,

N-succinimidyl [4-azidophenyl]-1,3'-dithiopropionate, N-succinimidyl [4-iodoacetyl]aminobenzoate, glutaraldehyde, formaldehyde and succinimidyl 4-[N-maleimidomethyl]cyclohexane-1-carboxylate.

[0068] The attachment site for binding to a multivalent entity may be naturally occurring, or may be introduced through genetic engineering. The site will be a specific binding pair member or one that is modified to provide a specific binding pair member, where the complementary pair has a multiplicity of specific binding sites. Binding to the complementary binding member can be a chemical reaction, epitope-receptor binding or hapten-receptor binding where a hapten is linked to the subunit chain. In a preferred embodiment, one of the subunits is fused to an amino acid sequence providing a recognition site for a modifying enzyme. The recognition sequence will usually be fused proximal to the carboxy terminus of one of the subunit to avoid potential hindrance at the antigenic peptide binding site. Conveniently, an expression cassette will include the sequence encoding the recognition site.

[0069] Modifying enzymes of interest include BirA, various glycosylases, farnesyl protein transferase, protein kinases and the like. The subunit may be reacted with the modifying enzyme at any convenient time, usually after formation of the monomer. The group introduced by the modifying enzyme, e.g. biotin, sugar, phosphate, farnesyl, etc. provides a complementary binding pair member, or a unique site for further modification, such as chemical cross-linking, biotinylation, etc. that will provide a complementary binding pair member. An alternative strategy is to introduce an unpaired cysteine residue to the subunit, thereby introducing a unique and chemically reactive site for binding. The attachment site may also be a naturally occurring or introduced epitope, where the multivalent binding partner will be an antibody, e.g. IgG, IgM, etc. Any modification will be at a site, e.g. C-terminal proximal, that will not interfere with binding.

[0070] Exemplary of multimer formation is the introduction of the recognition sequence for the enzyme BirA, which catalyzes biotinylation of the protein substrate. The monomer with a biotinylated subunit is then bound to a multivalent binding partner, e.g. streptavidin or avidin, to which biotin binds with extremely high affinity. Streptavidin has a valency of 4, providing a multimer of $(\alpha\text{-}\beta\text{-}P)_4$.

[0071] The multivalent binding partner may be free in solution, or may be attached to an insoluble support. Examples of suitable insoluble supports include beads, e.g. magnetic beads, membranes and microtiter plates. These are typically made of glass, plastic (e.g. polystyrene), polysaccharides, nylon or nitrocellulose. Attachment to an insoluble support is useful when the binding complex is to be used for separation of T cells.

[0072] Frequently, the multimeric complex will be labeled, so as to be directly detectable, or will be used in conjunction with secondary labeled immunoreagents which will specifically bind the complex. In general the label will have a light detectable characteristic. Preferred labels are fluorophors, such as fluorescein isothiocyanate (FITC), rhodamine, Texas Red, phycoerythrin and allophycocyanin. Other labels of interest may include dyes, enzymes, chemiluminescers, particles, radioisotopes, or other directly or indirectly detectable agent. Conveniently, the multivalent binding partner will have the labeling group. Alternatively, a second stage label may be used, e.g. labeled antibody directed to one of the peptide constituents, and the like.

[0073] The binding complex will be used to detect and/or separate antigen specific T cells. The T cells may be from any source, usually having the same species of origin as the MHC heterodimer. The T cells may be from an in vitro culture, or a physiologic sample. For the most part, the physiologic samples employed will be blood or lymph, but samples may also involve other sources oft cells, particularly where T cells may be invasive. Thus other sites of interest are tissues, or associated fluids, as in the brain, lymph node, neoplasms, spleen, liver, kidney, pancreas, tonsil, thymus, joints, synovia, and the like. The sample may be used as obtained or may be subject to modification, as in the case of dilution, concentration, or the like. Prior treatments may involve removal of cells by various techniques, including centrifugation, using Ficoll-Hypaque, panning, affinity separation, using antibodies specific for one or more markers present as surface membrane proteins on the surface of cells, or any other technique that provides enrichment of the set or subset of cells of interest.

[0074] The binding complex is added to a suspension comprising T cells of interest, and incubated at about 4° C for a period of time sufficient to bind the available cell surface receptor. The incubation will usually be at least about 5 minutes and usually

less than about 30 minutes. It is desirable to have a sufficient concentration of labeling reagent in the reaction mixture, so that labeling reaction is not limited by lack of labeling reagent. The appropriate concentration is determined by titration. The medium in which the cells are labeled will be any suitable medium as known in the art. If live cells are desired a medium will be chosen that maintains the viability of the cells. A preferred medium is phosphate buffered saline containing from 0.1 to 0.5% BSA. Various media are commercially available and may be used according to the nature of the cells, including Dulbecco's Modified Eagle Medium (dMEM), Hank's Basic Salt Solution (HBSS), Dulbecco's phosphate buffered saline (dPBS), RPMI, Iscove's medium, PBS with 5 mM EDTA, etc., frequently supplemented with fetal calf serum, BSA, HSA, etc.

[0075] Where a second stage labeling reagent is used, the cell suspension may be washed and resuspended in medium as described above prior to incubation with the second stage reagent. Alternatively, the second stage reagent may be added directly into the reaction mix.

[0076] A number of methods for detection and quantitation of labeled cells are known in the art. Flow cytometry is a convenient means of enumerating cells that are a small percent of the total population. Fluorescent microscopy may also be used. Various immunoassays, e.g. ELISA, RIA, etc. may used to quantitate the number of cells present after binding to an insoluble support.

[0077] Flow cyometry may also be used for the separation of a labeled subset of T cells from a complex mixture of cells. The cells may be collected in any appropriate medium which maintains the viability of the cells, usually having a cushion of serum at the bottom of the collection tube. Various media are commercially available as described above. The cells may then be used as appropriate.

[0078] Alternative means of separation utilize the binding complex bound directly or indirectly to an insoluble support, e.g. column, microtiter plate, magnetic beads, etc. The cell sample is added to the binding complex. The complex may be bound to the support by any convenient means. After incubation, the insoluble support is washed to remove non-bound components. From one to six washes may be employed, with sufficient volume to thoroughly wash non-specifically bound cells present in the sample. The desired cells are then eluted from the binding complex. In particular the use of

magnetic particles to separate cell subsets from complex mixtures is described in Miltenyi et al. (1990) Cytometry 11:231-238.

[0079] Detecting and/or quantitating specific T cells in a sample or fraction thereof may be accomplished by a variety of specific assays. In general, the assay will measure the binding between a patient sample, usually blood derived, generally in the form of plasma or serum and the subject multimeric binding complexes. The patient sample may be used directly, or diluted as appropriate, usually about 1:10 and usually not more than about 1:10,000. Assays may be performed in any physiological buffer, e.g. PBS, normal saline, HBSS, dPBS, etc.

[0080] A sandwich assay is performed by first attaching the multimeric binding complex to an insoluble surface or support. The multimeric binding complex may be bound to the surface by any convenient means, depending upon the nature of the surface, either directly or through specific antibodies. The particular manner of binding is not crucial so long as it is compatible with the reagents and overall methods of the invention. They may be bound to the plates covalently or non-covalently, preferably non-covalently.

[0081] The insoluble supports may be any compositions to which the multimeric binding complex can be bound, which is readily separated from soluble material, and which is otherwise compatible with the overall method of measuring T cells. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports to which the receptor is bound include beads, e.g. magnetic beads, membranes and microtiter plates. These are typically made of glass, plastic (e.g. polystyrene), polysaccharides, nylon or nitrocellulose. Microtiter plates are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples.

[0082] Before adding patient samples or fractions thereof, the non-specific binding sites on the insoluble support i.e. those not occupied by the multimeric binding complex, are generally blocked. Preferred blocking agents include non-interfering proteins such as bovine serum albumin, casein, gelatin, and the like. Samples, fractions or aliquots thereof are then added to separately assayable supports (for example, separate wells of a microtiter plate) containing support-bound multimeric binding complex.

[0083] Generally from about 0.001 to 1 ml of sample, diluted or otherwise, is sufficient, usually about 0.01 ml sufficing. Preferably, each sample and standard will be added to multiple wells so that mean values can be obtained for each. The incubation time should be sufficient for T cells to bind the insoluble binding complex. Generally, from about 0.1 to 3 hr is sufficient, usually 1 hr sufficing.

[0084] After incubation, the insoluble support is generally washed of non-bound components. Generally, a dilute physiologic buffer at an appropriate pH, generally 7-8, is used as a wash medium. From one to six washes may be employed, with sufficient volume to thoroughly wash non-specifically bound T cells present in the sample.

[0085] After washing, a solution containing specific second receptor is applied. The receptor may be any compound that binds patient T cells with sufficient specificity such that they can be distinguished from other components present. In a preferred embodiment, second receptors are antibodies specific for common T cell antigens, either monoclonal or polyclonal sera, e.g. anti-thy-1, anti-CD45, etc.

[0086] T cell specific antibodies may be labeled to facilitate direct or indirect quantification of binding. Examples of labels that permit direct measurement include radiolabels, such as ^{3}H or ^{125}I, fluorescers, dyes, beads, chemilumninescers, colloidal particles, and the like. Examples of labels which permit indirect measurement of binding include enzymes where the substrate may provide for a colored or fluorescent product. Examples of suitable enzymes for use in conjugates include horseradish peroxidase, alkaline phosphatase, malate dehydrogenase and the like. Where not commercially available, such antibody-enzyme conjugates are readily produced by techniques known to those skilled in the art.

[0087] Alternatively, the second receptor may be unlabeled. In this case, a labeled second receptor-specific compound is employed which binds to the bound second receptor. Such a second receptor-specific compound can be labelled in any of the above manners. It is possible to select such compounds such that multiple compounds bind each molecule of bound second receptor. Examples of second receptor/second receptor-specific molecule pairs include antibody/anti-antibody and avidin (or streptavidin)/biotin. Since the resultant signal is thus amplified, this technique may be advantageous where only a small number oft cells are present. An example is the use of a labeled antibody

specific to the second receptor. More specifically, where the second receptor is a rabbit anti-allotypic antibody, an antibody directed against the constant region of rabbit antibodies provides a suitable second receptor specific molecule. The anti-immunoglobulin will usually come from any source other than human, such as ovine, rodentia, particularly mouse, or bovine.

[0088] The volume, composition and concentration of T cell specific receptor solution provides for measurable binding to the T cells already bound to the insoluble substrate. Generally, the same volume as that of the sample is used: from about 0.001 to 1 ml is sufficient, usually about 0.1 ml sufficing. When antibody ligands are used, the concentration generally will be about 0.1 to 50 μg/ml, preferably about 1 μg/ml. The solution containing the second receptor is generally buffered in the range of about pH 6.5-9.5. The solution may also contain an innocuous protein as previously described. The incubation time should be sufficient for the labeled ligand to bind available molecules. Generally, from about 0.1 to 3 hr is sufficient, usually 1 hr sufficing.

[0089] After the second receptor or second receptor-conjugate has bound, the insoluble support is generally again washed free of non-specifically bound second receptor, essentially as described for prior washes. After non-specifically bound material has been cleared, the signal produced by the bound conjugate is detected by conventional means. Where an enzyme conjugate is used, an appropriate enzyme substrate is provided so a detectable product is formed. More specifically, where a peroxidase is the selected enzyme conjugate, a preferred substrate combination is H_2O_2 and O-phenylenediamine which yields a colored product under appropriate reaction conditions. Appropriate substrates for other enzyme conjugates such as those disclosed above are known to those skilled in the art. Suitable reaction conditions as well as means for detecting the various useful conjugates or their products are also known to those skilled in the art. For the product of the substrate O-phenylenediamine for example, light absorbance at 490-495 nm is conveniently measured with a spectrophotometer.

[0090] Generally the number of bound T cells detected will be compared to control samples from samples having a different MHC context, e.g. T cells from an animal that does not express the MHC molecule used to make the binding complex.

[0091] An alternative protocol is to provide anti-T cell reagent, e.g. anti-thy-1, anti-CD45, etc. bound to the insoluble surface. After adding the sample and washing away non-specifically bound T cells, one or a combination of the subject binding complexes are added, where the binding complexes are labeled so as not to interfere with the binding to T cells.

[0092] It is particularly convenient in a clinical setting to perform the assays in a self-contained apparatus. A number of such methods are known in the art. The apparatus will generally employ a continuous flow-path of a suitable filter or membrane, having at least three regions, a fluid transport region, a sample region, and a measuring region. The sample region is prevented from fluid transfer contact with the other portions of the flow path prior to receiving the sample. After the sample region receives the sample, it is brought into fluid transfer relationship with the other regions, and the fluid transfer region contacted with fluid to permit a reagent solution to pass through the sample region and into the measuring region. The measuring region may have bound to it the multimeric binding complex, with a conjugate of an enzyme with T cell specific antibody employed as a reagent, generally added to the sample before application. Alternatively, the binding complex may be conjugated to an enzyme, with T cell specific antibody bound to the measurement region.

[0093] Detection of T cells is of interest in connection with a variety of conditions associated with T cell activation. Such conditions include autoimmune diseases, e.g. multiple sclerosis, myasthenia gravis, rheumatoid arthritis, type 1 diabetes, graft vs. host disease, Grave's disease, etc.; various forms of cancer, e.g. carcinomas, melanomas, sarcomas, lymphomas and leukemias. Various infectious diseases such as those caused by viruses, e.g. HIV-1, hepatitis, herpesviruses, enteric viruses, respiratory viruses, rhabdovirus, rubeola, poxvirus, paramyxovirus, morbillivirus, etc. are of interest. Infectious agents of interest also include bacteria, such as Pneumococcus, Staphylococcus, Bacillus. Streptococcus, Meningococcus, Gonococcus, Eschericia, Klebsiella, Proteus, Pseudomonas, Salmonella, Shigella, Hemophilus, Yersinia, Listeria, Corynebacterium, Vibrio, Clostridia, Chlamydia, Mycobacterium, Helicobacter and Treponema; protozoan pathogens, and the like. T cell associated allergic responses may also be monitored, e.g. delayed type hypersensitivity or contact hypersensitivity involving T cells.

[0094] Of particular interest are conditions having an association with a specific peptide or MHC haplotype, where the subject binding complexes may be used to track the T cell response with respect to the haplotype and antigen. A large number of associations have been made in disease states that suggest that specific MHC haplotypes, or specific protein antigens are responsible for disease states.

[0095] Polypeptide fragments, including immunogenic fragments, for each of SEQ ID NOs: 1-27 can be any length from at least 5 consecutive amino acids to 1 amino acid less than a full length polypeptide of any given SEQ ID NO:. Thus, for SEQ ID NO: 1 (used here as a non-limiting example) the polypeptide fragment can contain any number of consecutive amino acids from 5 to 1903 (for example, 5, 6, 7, ... , 1901, 1902, 1903). For the sake of brevity, the individual integers between 5 and 1903 have not been reproduced herein but are, in fact, specifically contemplated. In one embodiment, the immunogenic fragments of the invention induce immunity or protective immunity from disease.

[0096] The present invention also provides for the exclusion of any individual fragment (of any given SEQ ID NO:) specified by N-terminal to C-terminal positions, actual sequence, or of any fragment specified by size (in amino acid residues) as described above. In addition, any number of fragments specified by N-terminal and C-terminal positions, actual sequence, or by size (in amino acid residues) as described above may be excluded as individual species. Further, any number of fragments specified by N-terminal and C-terminal positions or by size (in amino acid residues) as described above may be combined to provide a polypeptide fragment. These types of fragments may, optionally, include polypeptide sequences such as linkers, described below.

[0097] Where a claim recites "a polypeptide comprising SEQ ID NO: X, or fragments or immunogenic fragments or epitopes of SEQ ID NO:X", the language "fragments or immunogenic fragments or epitopes of SEQ ID NO:X" specifically excludes identical sub-sequences found within other longer naturally occurring prior art polypeptide or protein sequences that are not identical to sequence from which the claimed sequence was derived. This does not include instances where such sub-sequences are a part of a larger molecule specifically modified by the hand of man to enhance the immunogenicity of the fragments of the subject invention. Thus, fragments or immunogenic fragments or epitopes of SEQ ID NO:X specifically exclude, and are not

to be considered anticipated, where the fragment is a sub-sequence of another naturally occurring non-malarial peptide, polypeptide, or protein isolated from a bacterial, viral, reptilian, insect, avian, or mammalian source and is identified in a search of protein sequence databases.

[0098] Fragments or immunogenic fragments or epitopes of the invention may further contain linkers that facilitate the attachment of the fragments to a carrier molecule for the stimulation of an immune response or diagnostic purposes. The linkers can also be used to attach fragments according to the invention to solid support matrices for use in affinity purification protocols. In this aspect of the invention, the linkers specifically exclude, and are not to be considered anticipated, where the fragment is a subsequence of another peptide, polypeptide, or protein as identified in a search of protein sequence databases as indicated in the preceding paragraph. In other words, the non-identical portions of the other peptide, polypeptide, of protein are not considered to be a "linker" in this aspect of the invention. Non-limiting examples of "linkers" suitable for the practice of the invention include chemical linkers (such as those sold by Pierce, Rockford, IL) and peptides that allow for the connection of the immunogenic fragment to a carrier molecule (see, for example, linkers disclosed in U.S. Patent Nos. 6,121,424, 5,843,464, 5,750,352, and 5,990,275, hereby incorporated by reference in their entirety). In various embodiments, the linkers can be up to 50 amino acids in length, up to 40 amino acids in length, up to 30 amino acids in length, up to 20 amino acids in length, up to 10 amino acids in length, or up to 5 amino acids in length. Of course, the linker may be any pre-selected number of amino acids (up to 50 amino acids) in length.

[0099] In various embodiments, polypeptides suitable for use in various disclosed methods of the subject invention can be selected from the group consisting of: a) a polypeptide comprising a polypeptide sequence selected from the group consisting of SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16 ,17, 18, 19, 20, 21 ,22, 23, 24, 25, 26, and 27; b) a variant polypeptide having at least about 20% to 99.99% identity to a polypeptide selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16 ,17, 18, 19, 20, 21 ,22, 23, 24, 25, 26, and 27; c) a fragment of a polypeptide or a variant polypeptide of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16 ,17, 18, 19, 20, 21 ,22, 23, 24, 25, 26, or 27, wherein said fragment or variant

has substantially the same serologic reactivity or substantially the same T-cell reactivity as the native polypeptide; d) a multi-epitope construct; and e) combinations thereof.

Multi-epitope constructs

[00100] As indicated *supra*, the subject invention provides for "multi-epitope constructs". A "multi-epitope construct" comprises: 1) nucleic acids that encode multiple polypeptide epitopes (of any length) that can bind to one or more molecules functioning in the immune system; or 2) polypeptides comprising multiple polypeptide epitopes that can bind to one or more molecules functioning in the immune system. "Multi-epitope constructs" can, optionally, contain "flanking" or "spacing" residues between each epitope. Some embodiments provide for "multi-epitope constructs" that comprise a series of the same epitope (termed "homopolymers"). Other embodiments provide for "multi-epitope constructs" that comprise a combination or series of different epitopes, optionally connected by "flanking" or "spacing" residues (termed "heteropolymers"). In some embodiments, "multi-epitope constructs" may exclude full-length polypeptides from which the epitopes are obtained (*e.g.*, the polypeptides of SEQ ID NOs: 1-27). In certain preferred embodiments, the epitopes used in the formation of the multi-epitope construct are selected from those set forth in Table 2, Table 3, Table 4, Table 5, and/or Table 6 and any epitope set forth in these Tables 2-6 can be mixed and/or matched any other epitope set forth in any of the aforementioned Tables 2-6.

[00101] Multi-epitope constructs may be of "high affinity" or "intermediate affinity". As used herein, "high affinity" with respect to HLA class I molecules is defined as binding with an IC_{50}, or KD value, of 50 nM or less; "intermediate affinity" with respect to HLA class I molecules is defined as binding with an IC_{50} or KD value of between about 50 and about 500 nM. "High affinity" with respect to binding to HLA class II molecules is defined as binding with an IC_{50} or KD value of 100 nM or less; "intermediate affinity" with respect to binding to HLA class II molecules is defined as binding with an IC_{50} or KD value of between about 100 and about 1000 nM.

[00102] The multi-epitope constructs described herein preferably include five or more, ten or more, fifteen or more, twenty or more, or twenty-five or more epitopes. Other embodiments provide multi-epitope constructs that comprise at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33,

34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99 epitopes. All of the epitopes in a multi-epitope construct may be from one organism (*e.g.*, the epitopes are obtained from *P. falciparum*), or the multi-epitope construct may include epitopes present in two or more different organisms (*e.g.*, some epitopes from *P. falciparum* and some epitopes from another organism). Additionally, the same epitope may be present in a multi-epitope construct at more than one location in the construct. In some embodiments, novel epitopes of the subject invention may be linked to known epitopes of an organism (*e.g., P. falciparum* or another organism).

[00103] A "multi-epitope vaccine," is a vaccine comprising multiple epitopes. A multi-epitope vaccine can induce an immune response and is administered to an individual in an amount sufficient to induce an immune response in the individual. In some embodiments, the immune response induced by the multi-epitope vaccine is a protective immune response against a given organism, pathogen, or pathologic condition (*e.g.*, *P. falciparum*).

[00104] In certain embodiments, the epitopes of a multi-epitope construct or the polypeptides disclosed herein interact with an antigen binding site of an antibody molecule, a class I HLA, a T-cell receptor, and/or a class II HLA molecule. In certain preferred embodiments, the epitopes interact with an HLA molecule (*e.g.*, class I or class II) or a T-cell receptor. In an even more preferred embodiment, the epitope interacts with both an HLA molecule (*e.g.*, class I or class II) and a T-cell receptor. In various embodiments, all of the nucleic acids in a multi-epitope construct can encode class I HLA epitopes or class II HLA epitopes. Multi-epitope constructs comprising epitopes that interact exclusively with class I HLA molecules may be referred to as "CTL multi-epitope constructs" (or "$CD8^+$ T cell multi-epitope constructs"). Multi-epitope constructs comprising epitopes that interact exclusively with class II HLA molecules may be referred to as "HTL multi-epitope constructs" (or "$CD4^+$ T cell multi epitope constructs"). Some multi-epitope constructs (designated "TL multi-epitope constructs") can have a subset of the multi-epitope nucleic acids encoding class I HLA epitopes and another subset of the multi-epitope nucleic acids encoding class II HLA epitopes (*e.g.*, the constructs stimulate both CTL (*i.e.*, $CD8^+$ T cell) and HTL (*i.e.*, $CD4^+$ T cell) of the

immune system). Other multi-epitope constructs can provide epitopes that interact exclusively with B-cells or immunoglobulin molecules and are designated "BL multi-epitope constructs". Multi-epitope constructs that provide epitopes that interact with B-cells (and/or immunoglobulin molecules) and further provide class I HLA epitopes and class II HLA epitopes are designated "immune system (IMS) multi-epitope constructs". In certain embodiments, multi-epitope constructs can provide class I or class II epitopes (*e.g.*, CTL (*i.e.*, $CD8^+$ T cell) epitopes or HTL (*i.e.*, $CD4^+$ T cell) epitopes) and BL epitopes. "Human Leukocyte Antigen" or "HLA" is a human class I or class II Major Histocompatibility Complex (MHC) protein (see, *e.g.*, Stites, *et al.*, IMMUNOLOGY, 8^{TH} ED., Lange Publishing, Los Altos, Calif. (1994)).

[00105] CTL epitope (class I epitope) (*i.e.*, $CD8^+$ T cell epitope) encoding nucleic acids preferably provide an epitope peptide of about eight to about thirteen amino acids in length (*e.g.*, 8, 9, 10, 11, 12 or 13), more preferably about eight to about eleven amino acids in length, and most preferably about nine amino acids in length. HTL ($CD4^+$ T-cell) epitope nucleic acids can provide an epitope peptide of about seven to about twenty three (*e.g.*, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22 or 23) preferably about seven to about seventeen (*e.g.*, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17, more preferably about eleven to about fifteen (*e.g.*, 11, 12, 13, 14 or 15), and most preferably about thirteen amino acids in length.

[00106] "Degenerate binding" indicates that a peptide is bound by more than one HLA molecule; a synonym is "cross reactive binding." "Cross reactive binding" may also be used to define the interaction of an antigen with multiple populations of antibodies. In certain preferred embodiments, epitopes disclosed herein do not exhibit cross reactive or degenerate binding. Other embodiments encompass degenerate or cross reactive binding of antigens or epitopes.

[00107] With regard to a particular amino acid sequence, an "epitope" is a set of amino acid residues that is involved in recognition by a particular immunoglobulin, or in the context of T cells, those residues necessary for recognition by T cell receptor proteins and/or Major Histocompatibility Complex (MHC) receptors. In an immune system setting, *in vitro* or *in vivo*, an epitope is the collective features of a molecule, such as primary, secondary and tertiary peptide structure, and charge, that together form a site recognized by an immunoglobulin, T cell receptor or HLA molecule. Throughout this

disclosure epitope and peptide are often used interchangeably. It is to be appreciated, however, that isolated or purified protein or peptide molecules larger than and comprising an epitope of the invention are still within the bounds of the invention.

[00108] A "flanking" or "linking" residue is a residue that is positioned next to an epitope. A flanking residue can be introduced or inserted at a position adjacent to the N-terminus or the C-terminus of an epitope. Flanking residues suitable for use in the subject invention are disclosed, for example, in U.S. Patent Nos. 6,419,931, which is hereby incorporated by reference in its entirety, including all sequences, figures, references, and tables.

[00109] An "immunogenic peptide" or "peptide epitope" is a peptide that comprises an allele-specific motif or supermotif such that the peptide will bind an HLA molecule and induce a CTL (or $CD8^+$ T cell) and/or HTL (or $CD4^+$ T cell) response. An "immunogenic peptide" or "peptide epitope" can also be a peptide that comprises a motif that binds to antibody molecules or B-cells found in the immune system of an individual. Thus, immunogenic peptides of the invention are capable of binding to an antibody molecule, a B-cell, or appropriate HLA molecule and thereafter inducing an immune response (*e.g.*, the induction of antibody production, a cytotoxic T cell response, or a helper T cell response) to the antigen from which the immunogenic peptide is derived.

[00110] The term "residue" refers to an amino acid or amino acid mimetic incorporated into a peptide or protein by an amide bond or amide bond mimetic.

[00111] A "spacer" or "linker" refers to a sequence that is inserted between two epitopes in a multi-epitope construct to prevent the occurrence of junctional epitopes and/or to increase the efficiency of processing. A multi-epitope construct may have one or more spacer nucleic acids. A spacer nucleic acid may flank each epitope nucleic acid in a construct, or the spacer nucleic acid to epitope nucleic acid ratio may be about 2 to 10, about 5 to 10, about 6 to 10, about 7 to 10, about 8 to 10, or about 9 to 10, where a ratio of about 8 to 10 has been determined to yield favorable results for some constructs. The spacer nucleic acid may encode one or more amino acids. A spacer nucleic acid flanking a class I HLA epitope in a multi-epitope construct is preferably between one and about eight amino acids in length. A spacer nucleic acid flanking a class II HLA epitope in a multi-epitope construct is preferably greater than five, six, seven, or more amino acids in

length, and more preferably five or six amino acids in length. The number of spacers in a construct, the number of amino acids in a spacer, and the amino acid composition of a spacer can be selected to optimize epitope processing and/or minimize junctional epitopes. It is preferred that spacers are selected by concomitantly optimizing epitope processing and junctional motifs. Suitable amino acids for optimizing epitope processing are described herein. Also, suitable amino acid spacing for minimizing the number of junctional epitopes in a construct are described herein for class I and class II HLAs. For example, spacers flanking class II HLA epitopes preferably include G, P, and/or N residues as these are not generally known to be primary anchor residues (see, *e.g.*, PCT/US00/19774). A particularly preferred spacer for flanking a class II HLA epitope includes alternating G and P residues, for example, $(GP)_n$, $(PG)_n$, $(GP)_nG$, or $(PG)_nP$, and so forth, where n is an integer between one and ten, preferably two or about two, and where a specific example of such a spacer is GPGPG.

[00112] In some multi-epitope constructs, it is sufficient that each spacer nucleic acid encodes the same amino acid sequence. In multi-epitope constructs having two spacer nucleic acids encoding the same amino acid sequence, the spacer nucleic acids encoding those spacers may have the same or different nucleotide sequences, where different nucleotide sequences may be preferred to decrease the likelihood of unintended recombination events when the multi-epitope construct is inserted into cells.

[00113] In other multi-epitope constructs, one or more of the spacer nucleic acids may encode different amino acid sequences. While many of the spacer nucleic acids may encode the same amino acid sequence in a multi-epitope construct, one, two, three, four, five or more spacer nucleic acids may encode different amino acid sequences, and it is possible that all of the spacer nucleic acids in a multi-epitope construct encode different amino acid sequences. Spacer nucleic acids may be optimized with respect to the epitope nucleic acids they flank by determining whether a spacer sequence will maximize epitope processing and/or minimize junctional epitopes, as described herein.

[00114] Multi-epitope constructs may be distinguished from one another according to whether the spacers in one construct optimize epitope processing or minimize junctional epitopes over another construct, and preferably, constructs may be distinguished where one construct is concomitantly optimized for epitope processing and junctional epitopes over the other. Computer assisted methods and *in vitro* and *in vivo*

laboratory methods for determining whether a construct is optimized for epitope processing and junctional motifs are described herein.

[00115] "Multi-epitope constructs of the invention may also be "optimized". The term "optimized" or "optimizing" refers to increasing the immunogenicity or antigenicity of a multi-epitope construct having at least one epitope pair by sorting epitopes to minimize the occurrence of junctional epitopes, inserting flanking residues that flank the C-terminus or N-terminus of an epitope, and inserting spacer residue to further prevent the occurrence of junctional epitopes or to provide a flanking residue. An increase in immunogenicity or antigenicity of an optimized multi-epitope construct is measured relative to a multi-epitope construct that has not been constructed based on the optimization parameters and is using assays known to those of skill in the art, *e.g.*, assessment of immunogenicity in HLA transgenic mice, ELISPOT, interferon-gamma release assays, tetramer staining, chromium release assays, and presentation on dendritic cells.

[00116] The subject invention also concerns antibodies that bind to polypeptides of the invention. Antibodies that are immunospecific for the malarial polypeptides set forth herein are specifically contemplated. In various embodiments, antibodies which do not cross react with other proteins or malarial proteins are also specifically contemplated. The antibodies of the subject invention can be prepared using standard materials and methods known in the art (see, for example, *Monoclonal Antibodies: Principles and Practice*, 1983; *Monoclonal Hybridoma Antibodies: Techniques and Applications*, 1982; *Selected Methods in Cellular Immunology*, 1980; *Immunological Methods, Vol. II*, 1981; *Practical Immunology*, and Kohler *et al.* [1975] *Nature* 256:495).

[00117] The term "antibody" is used in the broadest sense and specifically covers monoclonal antibodies (including full length monoclonal antibodies), polyclonal antibodies, multispecific antibodies (*e.g.*, bispecific antibodies), and antibody fragments so long as they exhibit the desired biological activity, particularly neutralizing activity. "Antibody fragments" comprise a portion of a full length antibody, generally the antigen binding or variable region thereof. Examples of antibody fragments include Fab, Fab', $F(ab')_2$, and Fv fragments; diabodies; linear antibodies; single-chain antibody molecules; and multi-specific antibodies formed from antibody fragments.

[00118] The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, *i.e.*, the individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against a single antigenic site. Furthermore, in contrast to conventional (polyclonal) antibody preparations that typically include different antibodies directed against different determinants (epitopes), each monoclonal antibody is directed against a single determinant on the antigen. The modifier "monoclonal" indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies, and is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies to be used in accordance with the present invention may be made by the hybridoma method first described by Kohler *et al.* [1975] *Nature* 256: 495, or may be made by recombinant DNA methods (see, *e.g.*, U.S. Pat. No. 4,816,567). The "monoclonal antibodies" may also be isolated from phage antibody libraries using the techniques described in Clackson *et al.* [1991] *Nature* 352: 624-628 and Marks *et al.* [1991] *J. Mol. Biol.* 222: 581-597, for example.

[00119] The monoclonal antibodies described herein specifically include "chimeric" antibodies (immunoglobulins) in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired biological activity (U.S. Pat. No. 4,816,567; and Morrison *et al.* [1984] *Proc. Natl. Acad Sci. USA* 81: 6851-6855). Also included are humanized antibodies, such as those taught in U.S. Patent Nos. 6,407,213 or 6,417,337 which are hereby incorporated by reference in their entirety.

[00120] "Single-chain Fv" or "sFv" antibody fragments comprise the V_H and V_L domains of an antibody, wherein these domains are present in a single polypeptide chain. Generally, the Fv polypeptide further comprises a polypeptide linker between the V_H and V_L domains which enables the sFv to form the desired structure for antigen binding. For

a review of sFv see Pluckthun in The Pharmacology of Monoclonal Antibodies [1994] Vol. 113:269-315, Rosenburg and Moore eds. Springer-Verlag, New York.

[00121] The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy chain variable domain (V_H) connected to a light chain variable domain (V_L) in the same polypeptide chain (V_H -V_L). Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger *et al.* [1993] *Proc. Natl. Acad. Sci. USA* 90: 6444-6448. The term "linear antibodies" refers to the antibodies described in Zapata *et al.* [1995] *Protein Eng.* 8(10):1057-1062.

[00122] An "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody *in situ* within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

[00123] The terms "comprising", "consisting of" and "consisting essentially of" are defined according to their standard meaning. The terms may be substituted for one another throughout the instant application in order to attach the specific meaning associated with each term. The phrases "isolated" or "biologically pure" refer to material that is substantially or essentially free from components which normally accompany the material as it is found in its native state. Thus, isolated peptides in accordance with the invention preferably do not contain materials normally associated with the peptides in their *in situ* environment. "Link" or "join" refers to any method known in the art for functionally connecting peptides, including, without limitation, recombinant fusion,

covalent bonding, disulfide bonding, ionic bonding, hydrogen bonding, and electrostatic bonding.

[00124] Following are examples which illustrate procedures for practicing the invention. These examples should not be construed as limiting. All percentages are by weight and all solvent mixture proportions are by volume unless otherwise noted.

[00125] In this disclosure, "binding data" results are often expressed in terms of "IC_{50}'s." IC_{50} is the concentration of peptide in a binding assay at which 50% inhibition of binding of a reference peptide is observed. Given the conditions in which the assays are run (*i.e.*, limiting HLA proteins and labeled peptide concentrations), these values approximate KD values. Assays for determining binding are described in detail, *e.g.*, in PCT publications WO 94/20127 and WO 94/03205 (each of which is hereby incorporated by reference in its entirety). It should be noted that IC_{50} values can change, often dramatically, if the assay conditions are varied, and depending on the particular reagents used (*e.g.*, HLA preparation, etc.). For example, excessive concentrations of HLA molecules will increase the apparent measured IC_{50} of a given ligand. Alternatively, binding is expressed relative to a reference peptide. Although as a particular assay becomes more, or less, sensitive, the IC_{50}'s of the peptides tested may change somewhat, the binding relative to the reference peptide will not significantly change. For example, in an assay run under conditions such that the IC_{50} of the reference peptide increases 10-fold, the IC_{50} values of the test peptides will also shift approximately 10-fold. Therefore, to avoid ambiguities, the assessment of whether a peptide is a good, intermediate, weak, or negative binder is generally based on its IC_{50}, relative to the IC_{50} of a standard peptide. Binding may also be determined using other assay systems including those using: live cells (*e.g.*, Ceppellini *et al.*, Nature 339:392, 1989; Christnick *et al.*, Nature 352:67, 1991; Busch *et al.*, Int. Immunol. 2:443, 19990;Hill *et al.*, J. Immunol. 147:189,1991;del Guercio *et al.*, J. Immunol. 154:685, 1995), cell free systems using detergent lysates (*e.g.*, Cerundolo *et al.*, J. Immunol. 21:2069, 1991), immobilized purified MHC (*e.g.*, Hill *et al.*, J. Immunol. 152, 2890, 1994; Marshall *et al.*, J. Immunol. 152:4946, 1994), ELISA systems (*e.g.*, Reay *et al.*, EMBO J. 11:2829, 1992), surface plasmon resonance (*e.g.*, Khilko *et al.*, J. Biol. Chem. 268:15425, 1993); high flux soluble phase assays (Hammer *et al.*, J. Exp. Med. 180:2353, 1994), and measurement of class I MHC stabilization or assembly (*e.g.*, Ljunggren *et al.*, Nature 346:476, 1990; Schumacher *et al.*, Cell 62:563,

1990; Townsend *et al.*, Cell 62:285, 1990; Parker *et al.*, J. Immunol. 149:1896, 1992). Predicted IC_{50} values may be referred to as PIC values and measured IC_{50} values may be referred to a MIC values.

Example 1

[00126] Starting with 27 open reading frames defined by Multidimensional Protein Identification Technology, 9 highly antigenic proteins were identified. These highly antigenic proteins were recognized by volunteers immunized with irradiated sporozoites; mock immunized individuals (controls) failed to recognize these proteins. Several of these nine proteins were more antigenic than previously well-characterized proteins.

[00127] To identify and prioritize a set of ORFs representing antigens potentially expressed in the sporozoite and intrahepatic stage of the parasite life cycle, MS/MS spectra of peptide sequences generated by Multidimensional Protein Identification Technology (MudPIT) (Washburn, M.P., Wolters, D., & Yates, J.R. 3rd. Large-scale analysis of the yeast proteome by multidimensional protein identification technology. *Nat. Biotechnol.* 19, 242-247 (2001)) of *P. falciparum* sporozoite preparations were scanned against the *P. falciparum* genomic sequence database using SEQUEST™ software (Florens, L. *et al.* A proteomic view of the *Plasmodium falciparum* life cycle. *Submitted*). A panel of 27 ORF's (10 expressed only in sporozoites, and 17 common to other stages of the parasite life cycle) were selected. Their size ranged between 96 - 4544 amino acids (mean 1252), the percentage of the protein covered by identified peptides ranged between 0.5 - 49.5%, and the frequency of recognition in the *P. falciparum* proteome dataset ranged between 16 peptide hits from 6 different sporozoite runs (antigen 2) to single peptide hits (antigens 1, 11, 14, 16, 19 and 25. When searched against the final *P. falciparum* database using refined gene model predictions, and taking into consideration genomic sequence information from the *Anopheles* (vector) and human (host) databases, 19 of the 27 antigens could be identified using stringent selection criteria and six others could be identified only with relaxed criteria.

[00128] Amino acid sequences from the 27 ORFs were scanned with HLA-A1, A2, A3/A11, A24 and DR supertype PIC algorithms; a total of 3241 peptides were identified (range = 14-435; mean = 120 sequences per antigen). A set of 1142 sequences was synthesized (range = 13-50; mean = 42), selecting the top 10 scorers per supertype

per antigen for larger ORFs. Control sets of peptides were synthesized from 4 known antigens (PfCSP, PfSSP2, PfLSA1 and PfEXP1). Next, predicted epitopes were tested for their capacity to induce recall IFN-γ immune responses using PBMC from volunteers immunized with irradiated *P. falciparum* sporozoites and either protected (n=4) or not protected (n=4) against challenge with infectious sporozoites, or control volunteers mock immunized in parallel (n=4) (see Table 1). Peptides were tested as pools, at 1 μg/ml each peptide with each antigen represented by a separate pool, by IFN-γ ELIspot (Washburn, M.P., Wolters, D., &Yates, J.R. 3rd. Large-scale analysis of the yeast proteome by multidimensional protein identification technology. *Nat. Biotechnol.* **19**, 242-247 (2001)). Positive and negative control epitopes from well characterized antigens (CMV, Influenza, EBV, HIV) were also included.

[00129] Considering a stimulation index (ratio test response/control) > 2.0 as positive, 19 of the 27 unknown antigens were recognized by at least 1 of 8 irradiated sporozoite immunized volunteers, but not by any of the 4 mock immunized controls (Table 1). Nine of the 27 antigens (#2, 5, 3, 18, 22, 21, 13, 11, 20) were recognized by at least 50% of irradiated sporozoite volunteers in at least 25% of assays, 3 antigens (#1, 12, 17) were recognized by at least 25% of volunteers in at least 15% of assays, and 7 antigens (#6, 7, 9, 14, 15, 16, 19) were recognized by at least 10% volunteers in at least 5% of assays. Eight of the 27 unknown antigens (#4, 8, 10, 23, 24, 25, 26, 27) failed to induce IFN-γ responses of sufficient magnitude to meet our criteria of positivity. Pools of predicted epitopes from the known antigens, PfCSP, PfSSP2, PfLSA1 and PfEXP1, were also recognized by irradiated sporozoite volunteers although the frequency of response to those pools was somewhat lower than that to pools of peptides representing previously validated epitopes derived from the same antigens (Doolan, D.L. *et al.* Degenerate cytotoxic T cell epitopes from P. falciparum restricted by multiple HLA-A and HLA-B supertype alleles. Immunity. 7, 97-112 (1997); Doolan, D.L. *et al.* HLA-DR-promiscuous T cell epitopes from *Plasmodium* flaciparum pre-erthrocytic-stage antigens restricted by multiple HLA class II alleles. J Immunol. 165:1123-1137 (2000); Wang, R., *et al.* Induction of CD4(+) T cell-dependent CD8(+) type 1 responses in humans by a malaria DNA vaccine. *Proc. Natl. Acad. Sci. U.S.*A. **98**, 10817-10822 (2001)) (Table 1). Particularly noteworthy, the reactivity against several of the newly identified antigens greatly exceeded the reactivities observed against all 4 known antigens For example, both

antigens 2 and 5 were recognized by 7/8 irradiated sporozoite volunteers in 9/16 assays, and antigens 3 and 18 were recognized by 6/8 irradiated sporozoite volunteers in 6/16 assays.

[00130] Results show that HLA-A2 peptide pools from antigens 2, 5 and 13, and HLA-A1 and HLA-DR peptide pools from antigens 2 and 5, are recognized by irradiated sporozoite volunteers who express the respective HLA alleles, but not by mock immunized controls. Deconvolution at the level of individual epitopes is in progress. Additionally, a comprehensive analysis of HLA binding against the A1, A2, A3/11, A24, and DR1 supertypes has been completed for selected antigens. Several degenerate binders have been identified for each supertype/antigen combination, and 50 to 70% of the predicted peptides have been identified as degenerate HLA binders.Further analysis also revealed that the antigenicity results correlate to a large degree with the proteomic data. For example, of 9 antigens associated with high immune reactivity, 7 were identified by multiple peptide hits in multiple MudPIT runs

[00131] All patents, patent applications, provisional applications, polynucleotide sequences, amino acid sequences, tables and publications referred to or cited herein are incorporated by reference in their entirety, including all figures, to the extent they are not inconsistent with the explicit teachings of this specification. It should be understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application.

Table 1. Summary of immune reactivities against the panel of 27 putative antigens and 4 known antigens.

Antigen	IRRADIATED SPOROZOITE IMMUNIZED						MOCK IMMUNIZED	
	# vol respond	% vol respond	# assays	% assays	SI respond	SFC respond	# vol respond	# assays
1	3	37.5	3	18.75	2.5	59.3	0	0
2	8	100	9	56.25	2.9	110.4	0	0
3	6	75	6	37.5	2.6	119.1	0	0
4	0	-	-	-	-	-	0	0
5	7	87.5	9	56.25	2.8	101.8	0	0
6	1	12.5	1	6.25	2.4	88.3	0	0
7	1	12.5	1	6.25	2.1	43.3	0	0
8	0	-	-	-	-	-	0	0
9	2	25	2	12.5	2.5	32.0	0	0
10	0	-	-	-	-	-	0	0
11	4	50	4	25	3.1	81.3	0	0
12	3	37.5	3	18.75	2.2	48.2	0	0
13	4	50	5	31.25	2.9	92.2	0	0
14	1	12.5	1	6.25	2.2	55.3	0	0
15	2	25	2	12.5	2.5	28.8	0	0
16	2	25	2	12.5	2.2	27.2	0	0
17	3	37.5	3	18.75	2.4	57.6	0	0
18	6	75	6	37.5	2.2	58.4	0	0
19	2	25	2	12.5	2.7	31.3	0	0
20	4	50	4	25	2.5	74.8	0	0
21	4	50	5	31.25	2.3	48.2	0	0
22	5	62.5	5	31.25	2.9	108.4	0	0
23	0	-	-	-	-	-	0	0
24	0	-	-	-	-	-	0	0
25	0	-	-	-	-	-	0	0
26	0	-	-	-	-	-	0	0
27	0	-	-	-	-	-	0	0
TOTAL UNKNOWNS	1-8	44.7	3.8	24.0	2.5	66.6		
"HIGH"	4-8	66.7	5.9	36.8	2.7	88.3		
"INTERMEDIATE"	3	37.5	3.0	18.8	2.4	55.0		
"LOW"	1-2	19.6	1.6	9.8	2.4	43.8		
Range	1-8	12.5-100	1-9	6.25-56.25	2.1-3.1	27.2-110.4		
KNOWNS (@1ug/ml) predicted	1.4	17.2	1.4	8.6	2.9	57.3		
Range	1-3	12.5-37.5	1-3	6.25-18.75	2.0-3.4	30.5-137.4		
KNOWNS (@1ug/ml) validated	4.0	50.0	3.8	23.4	3.5	64.0		
Range	3-5	37.5-62.5	3-6	18.75-37.5	3.5-3.6	46.6-91.4		
TOTAL KNOWNS (@1ug/ml)	2.3	28.1	2.2	13.5	3.2	60.0		
Range	1-5	12.5-62.5	1-6	6.25-37.5	2.0-3.6	30.5-137.4		
TOTAL KNOWNS (@10ug/ml)	4-8	81.3	7.8	60.9	11.1	588.2		
CMV/EBV/Flu	7	87.5	12.0	50.0	4.0	59.0	4	100

Table 2:
Pf-derived A1 supertype peptides with PIC <20nM

Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	PIC A*0101 PIC	A*0201	A*1101	A*2402 PIC
331.t00003	Chromosome10		216	98.0038	KTNKWEDIY	9	15.962	1000000.0	1475.7	1000000.0
331.t00003	Chromosome10		790	98.0039	KSIYIFYTY	9	10.624	1000000.0	34.6	1000000.0
331.t00003	Chromosome10		986	98.0040	GTFTFQNMY	9	6.439	1000000.0	51.0	1000000.0
331.t00003	Chromosome10		1298	98.0041	CNDGNILYY	9	5.246	1000000.0	1000000.0	1000000.0
331.t00003	Chromosome10		1379	98.0042	YFECIMKLY	9	8.786	1000000.0	39035.2	242.6
331.t00003	Chromosome10		1389	98.0043	VYEGKLKKY	9	18.802	1000000.0	1000000.0	1753.1
331.t00003	Chromosome10		1650	98.0001	VVDLFCGVGY	10	9.498	1000000.0	153.7	1000000.0
331.t00003	Chromosome10		1770	98.0044	FSSINTYDY	9	4.161	1000000.0	4680.1	1000000.0
331.t00003	Chromosome10		1803	98.0045	VSNVEDSNY	9	18.299	1000000.0	11308.4	1000000.0
331.t00003	Chromosome10		1831	98.0046	NSNYNKKLY	9	19.200	1000000.0	4533.0	1000000.0
18.000811	Chr12Contig18		182	98.0047	KVSDEIWNY	9	6.117	1000000.0	40.5	1000000.0
MY924Fe3.pltl			92	98.0048	ISGEGLIIY	9	4.901	1000000.0	2464.4	1000000.0
MY924Fe3.pltl			215	98.0002	FVEDSSSFLY	10	8.740	1000000.0	445.2	1000000.0
MY924Fe3.pltl			384	98.0049	DSDSSNVLY	9	7.960	1000000.0	22156.1	1000000.0
MY924Fe3.pltl			561	98.0050	SQDVFIIEY	9	6.978	1000000.0	117.2	1000000.0
MY924Fe3.pltl			1028	98.0051	NSMFHIIMY	9	4.429	1000000.0	243.3	1000000.0
MY924Fe3.pltl			1093	98.0052	SSYNLFEEY	9	6.022	1000000.0	82.2	1000000.0
MY924Fe3.pltl			1258	98.0053	SSGKTFICY	9	2.145	1000000.0	264.3	1000000.0
MY924Fe3.pltl			1340	98.0054	ILENILLSY	9	3.307	1000000.0	8368.7	1000000.0
MY924Fe3.pltl			1439	98.0055	FSDLILYVY	9	2.218	1000000.0	4308.8	1000000.0
MY924Fe3.pltl			2318	98.0056	HIENILLKY	9	2.560	1000000.0	10911.0	1000000.0
MP03001	MAL3P2.11	CAB38998	14	98.0057	FVEALFQEY	9	1.370	1000000.0	698.4	1000000.0
MP03001	MAL3P2.11	CAB38998	310	98.0058	PSDKHIKEY	9	18.149	1000000.0	150075.4	1000000.0
1369.t00001	Chromosome 11		38	98.0059	IMNHLMTLY	9	9.966	1000000.0	224.2	1019.1
1369.t00001	Chromosome 11		149	98.0060	LIENELMNY	9	18.117	1000000.0	15763.1	1000000.0
1369.t00001	Chromosome 11		182	98.0061	NVDQQNDMY	9	6.934	1000000.0	6419.6	1000000.0
1369.t00001	Chromosome 11		309	98.0062	SSFFMNRFY	9	17.546	1000000.0	48.4	1000000.0
1369.t00001	Chromosome 11		342	98.0063	NHEQKLSEY	9	16.912	1000000.0	1000000.0	1000000.0

Table 2:
Pf-derived A1 supertype peptides with PIC <20nM

Docket No.: EPI-103X

Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	PIC A*0101 PIC	A*0201	A*1101	A*2402 PIC
1369.t00001	Chromosome 11		347	98.0003	LSEYYDXDIY	10	18.838	1000000.0	3608.2	1000000.0
1369.t00001	Chromosome 11		363	98.0064	QEEQKKYIY	9	19.642	1000000.0	1000000.0	1000000.0
699.t00001	Chromosome 11		313	98.0065	DSQNELTNY	9	19.647	1000000.0	97274.6	1000000.0
699.t00001	Chromosome 11		441	98.0004	FSFFFSLIDY	10	1.491	1000000.0	319.3	1000000.0
699.t00001	Chromosome 11		480	98.0066	CHEMKAEFY	9	15.998	1000000.0	1000000.0	1000000.0
699.t00001	Chromosome 11		548	98.0067	MFSSIFENY	9	6.908	1000000.0	1357.8	2826.7
699.t00001	Chromosome 11		749	98.0068	NSLILLNLY	9	11.791	1000000.0	4626.8	1000000.0
699.t00001	Chromosome 11		859	98.0069	YIDNDINIY	9	12.867	1000000.0	52350.4	1000000.0
699.t00001	Chromosome 11		919	98.0070	EEDKTYELY	9	13.159	1000000.0	1000000.0	1000000.0
699.t00001	Chromosome 11		922	98.0071	KTYELYQKY	9	7.495	1000000.0	22.4	1000000.0
699.t00001	Chromosome 11		1013	98.0072	CTHISYYKY	9	14.092	1000000.0	406.1	1000000.0
699.t00001	Chromosome 11		1046	98.0005	FVDEEGEQLY	10	6.559	1000000.0	5771.7	1000000.0
M13Hg2.q1t3			8	98.0073	NSLYNKIEY	9	19.553	1000000.0	3889.9	1000000.0
M13Hg2.q1t3			46	98.0006	YSSASESNFY	10	12.365	1000000.0	5058.0	1000000.0
M13Hg2.q1t3			49	98.0074	ASESNFYKY	9	1.848	1000000.0	630.5	1000000.0
M13Hg2.q1t3			196	98.0075	ASGKLFSLY	9	2.466	1000000.0	266.9	1000000.0
M13Hg2.q1t3			237	98.0076	GSNKVSDWY	9	16.782	1000000.0	1646.1	1000000.0
M13Hg2.q1t3			511	98.0007	FQDNYLKLDY	10	7.493	1000000.0	19742.1	1000000.0
M13Hg2.q1t3			597	98.0008	FFDYNSQYYY	10	19.854	1000000.0	2749.2	1043.1
M13Hg2.q1t3			597	98.0077	FFDYNSQYY	9	11.735	1000000.0	3766.2	160.3
M13Hg2.q1t3			699	98.0078	MLEQKLSNY	9	1.204	1000000.0	13925.8	1000000.0
M13Hg2.q1t3			882	98.0079	NSFNNSNIY	9	16.821	1000000.0	5231.6	1000000.0
Mal_5L10c4.q1t6			8	98.0080	CSSTKDLNY	9	2.097	1000000.0	16168.9	1000000.0
Mal_5L10c4.q1t6			263	98.0081	YDDDKYNKY	9	7.997	1000000.0	98918.2	1000000.0
Mal_5L10c4.q1t6			638	98.0082	GTYGNMENY	9	2.825	1000000.0	209.0	1000000.0
Mal_5L10c4.q1t6			690	98.0083	FTYYSCKNY	9	6.979	1000000.0	257.7	1000000.0
Mal_5L10c4.q1t6			1022	98.0084	YDERNTLVY	9	5.181	1000000.0	47876.1	1000000.0
Mal_5L10c4.q1t6			1387	98.0085	STDDSKNVY	9	4.783	1000000.0	2220.4	1000000.0

Table 2:
Pf-derived A1 supertype peptides with PIC <20nM

Docket No.: EPI-103X

Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	PIC A*0101 PIC	A*0201	A*1101	A*2402 PIC
Mal_5L10c4.q1t6			1451	98.0086	FSDDNKNLY	9	2.622	1000000.0	56737.7	1000000.0
Mal_5L10c4.q1t6			1508	98.0009	YLDNELTINY	10	6.162	1000000.0	7177.6	1000000.0
Mal_5L10c4.q1t6			1709	98.0087	STTSLNYHY	9	7.670	1000000.0	19.1	1000000.0
Mal_5L10c4.q1t6			1907	98.0088	GLDLKMTLY	9	2.747	1000000.0	5170.0	1000000.0
571.t00003	Chromosome11		1044	98.0010	YTFQNNNDFY	10	2.179	1000000.0	93.5	1000000.0
571.t00003	Chromosome11		1080	98.0089	HTNNKTSIY	9	4.189	1000000.0	1677.3	1000000.0
571.t00003	Chromosome11		1710	98.0090	FVDPNKYIY	9	2.171	1000000.0	6898.3	1000000.0
571.t00003	Chromosome11		1827	98.0011	NVEAYHNDNY	10	5.835	1000000.0	1804.6	1000000.0
571.t00003	Chromosome11		1858	98.0091	YSNNSHAEY	9	7.282	1000000.0	662.3	1000000.0
571.t00003	Chromosome11		1905	98.0092	LTNNSSYIY	9	7.415	1000000.0	186.2	1000000.0
571.t00003	Chromosome11		2211	98.0093	SSSIYNQNY	9	6.330	1000000.0	318.5	1000000.0
571.t00003	Chromosome11		2476	98.0094	GSYGTFLKY	9	1.127	1000000.0	151.7	1000000.0
571.t00003	Chromosome11		2532	98.0095	DIDKTVLHY	9	4.678	1000000.0	10960.5	1000000.0
571.t00003	Chromosome11		2571	98.0012	FNDTQKKGTY	10	7.668	1000000.0	1000000.0	1000000.0
MP03072	PFC0450w	CAA15614	95	98.0013	LSASDEYEQY	10	14.664	1000000.0	11938.7	1000000.0
MP03072	PFC0450w	CAA15614	96	98.0096	SASDEYEQY	9	16.603	1000000.0	163.8	1000000.0
45.t00001	Chromosome14		13	98.0014	FQAAESNERY	10	13.667	1000000.0	5804.6	1000000.0
45.t00001	Chromosome14		14	98.0097	QAAESNERY	9	7.537	1000000.0	4581.2	1000000.0
45.t00001	Chromosome14		81	98.0015	ELEASISGKY	10	17.550	1000000.0	30954.5	1000000.0
45.t00001	Chromosome14		82	98.0098	LEASISGKY	9	18.208	1000000.0	1000000.0	1000000.0
45.t00001	Chromosome14		188	98.0099	NLALLYGEY	9	12.836	1000000.0	4104.6	1000000.0
MP03137	PFC0700c	CAB11150	14	98.0100	SSPLFNNFY	9	20.002	1000000.0	464.0	1000000.0
MP03137	PFC0700c	CAB11150	69	98.0101	LNEQLIYTY	9	10.436	1000000.0	1000000.0	1000000.0
MP03137	PFC0700c	CAB11150	145	98.0102	QNADKNFLY	9	10.234	1000000.0	1000000.0	1000000.0
MP03137	PFC0700c	CAB11150	255	98.0016	FVSSIFISFY	10	10.460	1000000.0	44.6	1000000.0
MP03137	PFC0700c	CAB11150	256	98.0103	VSSIFISFY	9	15.732	1000000.0	544.5	1000000.0
12.t00018	Chromosome14		112	98.0104	YSYYEPLRY	9	4.229	1000000.0	560.9	1000000.0
12.t00018	Chromosome14		250	98.0017	KSNNIIPLLY	10	8.533	1000000.0	967.3	1000000.0

Table 2:
Pf-derived A1 supertype peptides with PIC <20nM

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Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	PIC A*0101 PIC	A*0201	A*1101	A*2402 PIC
12.t00018	Chromosome14		467	98.0105	SSSDEENLY	9	8.006	1000000.0	2243.6	1000000.0
12.t00018	Chromosome14		468	98.0106	SSDEENLYY	9	6.105	1000000.0	64.6	1000000.0
12.t00018	Chromosome14		607	98.0107	KSNMNNNLY	9	6.927	1000000.0	923.1	1000000.0
12.t00018	Chromosome14		626	98.0108	FYDKRFIFY	9	4.639	1000000.0	1000000.0	18.3
12.t00018	Chromosome14		696	98.0018	NVEKNFLLYY	10	7.724	1000000.0	328.7	1000000.0
12.t00018	Chromosome14		696	98.0109	NVEKNFLLY	9	0.789	1000000.0	1330.7	1000000.0
12.t00018	Chromosome14		949	98.0110	KMDSFLNVY	9	6.016	1000000.0	1384.3	151.9
12.t00018	Chromosome14		1042	98.0111	NSLIEFLFY	9	9.105	1000000.0	774.9	1000000.0
mal_BU121g9.q1c1			80	98.0112	ATYKNGNIY	9	3.423	1000000.0	290.6	1000000.0
mal_9A57b11.q1t2			226	98.0113	DEEKIFVKY	9	18.436	1000000.0	1000000.0	1000000.0
mal_BL50e8.p1ca_5			86	98.0114	HTSNDSGSY	9	7.801	1000000.0	10632.6	1000000.0
mal_BL50e8.p1ca_5			136	98.0019	FSFTVGEGKY	10	4.464	1000000.0	4191.1	1000000.0
mal_BL50e8.p1ca_5			186	98.0115	ETNNNLFIY	9	3.940	1000000.0	574.3	1000000.0
mal_BL50e8.p1ca_5			319	98.0116	HVSKHAFEY	9	3.473	1000000.0	286.4	1000000.0
mal_BL50e8.p1ca_5			387	98.0117	MSGYSSNNY	9	4.983	1000000.0	1178.7	1000000.0
mal_BL50e8.p1ca_5			460	98.0118	FMESAFVNY	9	2.609	1000000.0	3568.1	1208.1
mal_BL50e8.p1ca_5			650	98.0119	RSPCSHKLY	9	6.243	1000000.0	805.6	1000000.0
mal_BL50e8.p1ca_5			679	98.0020	FTGENNIERY	10	15.909	1000000.0	1908.1	1000000.0
mal_BL50e8.p1ca_5			777	98.0120	NTLMLKADY	9	15.648	1000000.0	6774.7	1000000.0
mal_BL50e8.p1ca_5			880	98.0121	VSSKPANEY	9	15.176	1000000.0	3405.9	1000000.0
M13S8h6.p1t_3			57	98.0122	ITYSFTVSY	9	10.960	1000000.0	25.1	1000000.0
M13S8h6.p1t_3			233	98.0123	LVETLDNLY	9	3.907	1000000.0	24044.7	1000000.0
M13S8h6.p1t_3			235	98.0124	ETLDNLYLY	9	2.901	1000000.0	801.6	1000000.0
M13S8h6.p1t_3			295	98.0125	LSAKYYISY	9	4.669	1000000.0	635.7	1000000.0
M13S8h6.p1t_3			551	98.0126	HSDIHLLNY	9	1.423	1000000.0	5008.9	1000000.0
M13S8h6.p1t_3			676	98.0021	FTSPVNIKEY	10	10.972	1000000.0	1911.2	1000000.0
M13S8h6.p1t_3			746	98.0127	YSSYSSPKY	9	5.286	1000000.0	6184.9	1000000.0
M13S8h6.p1t_3			898	98.0128	GMERNKTKY	9	7.244	1000000.0	88038.7	24764.5

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Pf-derived A1 supertype peptides with PIC <20nM

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M13S8h6.plt_3			1268	98.0129	YSNIDSGKY	9	11.517	1000000.0	14325.6	1000000.0
M13S8h6.plt_3			1488	98.0130	LIDLSCIHY	9	3.960	1000000.0	1722.8	1000000.0
585.t00002	Chromosome11		297	98.0131	CSDSSLNIY	9	2.643	1000000.0	44436.7	1000000.0
585.t00002	Chromosome11		381	98.0132	VSFDNNENY	9	7.080	1000000.0	824.4	1000000.0
585.t00002	Chromosome11		465	98.0022	YTDIIINIRY	10	1.851	1000000.0	1716.6	1000000.0
585.t00002	Chromosome11		575	98.0023	LSNIRKPLFY	10	5.132	1000000.0	3669.8	1000000.0
585.t00002	Chromosome11		741	98.0133	NVDANYCKY	9	3.822	1000000.0	813.1	1000000.0
585.t00002	Chromosome11		1021	98.0134	CVEKNNMSY	9	6.497	1000000.0	33246.6	1000000.0
585.t00002	Chromosome11		1161	98.0135	SSDGKKSEY	9	5.530	1000000.0	8369.5	1000000.0
585.t00002	Chromosome11		1219	98.0136	RSNNFFFSY	9	6.117	1000000.0	11.9	1000000.0
585.t00002	Chromosome11		1361	98.0024	FTMVYEKIKY	10	2.669	1000000.0	726.8	1000000.0
585.t00002	Chromosome11		1739	98.0137	NVDIFLHYY	9	3.691	1000000.0	42.6	1000000.0
1223.t00015	mal_9A21f9.qlt_4		387	98.0138	SSNEIHNFY	9	7.488	1000000.0	19.5	1000000.0
1223.t00015	mal_9A21f9.qlt_4		1065	98.0139	GTKLNRTKY	9	6.438	1000000.0	9805.4	1000000.0
1223.t00015	mal_9A21f9.qlt_4		1583	98.0025	ATVSRAGIVY	10	9.716	1000000.0	351.9	1000000.0
1223.t00015	mal_9A21f9.qlt_4		1833	98.0140	YTLSSGTKY	9	4.847	1000000.0	1878.1	1000000.0
1223.t00015	mal_9A21f9.qlt_4		2309	98.0141	VSEKEQQLY	9	6.585	1000000.0	56024.7	1000000.0
1223.t00015	mal_9A21f9.qlt_4		2426	98.0142	VVDFERLRY	9	3.185	1000000.0	457.2	1000000.0
1223.t00015	mal_9A21f9.qlt_4		2778	98.0143	FIDLYKQMY	9	5.792	1000000.0	14889.5	1000000.0
1223.t00015	mal_9A21f9.qlt_4		3445	98.0144	IVDITNVNY	9	6.389	1000000.0	1065.1	1000000.0
1223.t00015	mal_9A21f9.qlt_4		4163	98.0145	LEDVKKILY	9	9.183	1000000.0	1000000.0	1000000.0
1223.t00015	mal_9A21f9.qlt_4		4267	98.0146	SLDIPDIAY	9	9.566	1000000.0	1095.4	1000000.0
599.t00001	Chromosome11		26	98.0147	SSCQNSLNY	9	1.030	1000000.0	86.7	1000000.0
599.t00001	Chromosome11		183	98.0148	KSDITNLNY	9	4.923	1000000.0	947.1	1000000.0
599.t00001	Chromosome11		304	98.0149	ETNNGDLKY	9	6.392	1000000.0	6561.2	1000000.0
599.t00001	Chromosome11		430	98.0150	LSEDNKNRY	9	7.171	1000000.0	178412.8	1000000.0
599.t00001	Chromosome11		1018	98.0026	LLDLRKNGLY	10	3.696	1000000.0	12286.3	1000000.0
599.t00001	Chromosome11		1412	98.0027	GVDKSLKIMY	10	8.185	1000000.0	3010.4	1000000.0

Table 2:
Pf-derived A1 supertype peptides with PIC <20nM

Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	PIC A*0101 PIC	A*0201	A*1101	A*2402 PIC
599.t00001	Chromosome11		1427	98.0151	YTPTNKEMY	9	6.553	1000000.0	73406.9	1000000.0
599.t00001	Chromosome11		1516	98.0028	ESANDSTNYY	10	6.672	1000000.0	2007.1	1000000.0
599.t00001	Chromosome11		1662	98.0152	LSNSITVSY	9	9.278	1000000.0	771.6	1000000.0
599.t00001	Chromosome11		1902	98.0153	GTTQSNNIY	9	3.444	1000000.0	4003.2	1000000.0
MP01072	M1045c5.plc.C_6		27	98.0154	SDDEIIIIY	9	11.359	1000000.0	1265.6	1000000.0
MP01072	M1045c5.plc.C_6		41	98.0155	ISSNGKLNY	9	6.926	1000000.0	2877.4	1000000.0
MP01072	M1045c5.plc.C_6		60	98.0156	GSIQNAYLY	9	2.697	1000000.0	389.5	1000000.0
MP01072	M1045c5.plc.C_6		381	98.0157	GTMRNRKKY	9	1.998	1000000.0	249.1	1000000.0
MP01072	M1045c5.plc.C_6		707	98.0158	KSLLKNYNY	9	15.958	1000000.0	419.1	1000000.0
MP01072	M1045c5.plc.C_6		725	98.0159	NVEDTNMLY	9	9.314	1000000.0	3255.4	1000000.0
MP01072	M1045c5.plc.C_6		1065	98.0029	NTDNKDVLNY	10	6.923	1000000.0	6127.0	1000000.0
MP01072	M1045c5.plc.C_6		1253	98.0160	HTITISQKY	9	3.528	1000000.0	4947.2	1000000.0
MP01072	M1045c5.plc.C_6		1257	98.0161	ISQKYTSSY	9	13.157	1000000.0	5019.1	1000000.0
MP01072	M1045c5.plc.C_6		1336	98.0030	KTFHRILAVY	10	13.836	1000000.0	85.1	1000000.0
PIR2	T28161		228	98.0162	KTNGAEERY	9	8.691	1000000.0	326.3	1000000.0
PIR2	T28161		293	98.0163	GTVPTNLDY	9	3.979	1000000.0	793.4	1000000.0
PIR2	T28161		403	98.0031	ESSQNSPKNY	10	8.536	1000000.0	24883.8	1000000.0
PIR2	T28161		639	98.0032	QTDFQGWGHY	10	2.601	1000000.0	1349.4	1000000.0
PIR2	T28161		899	98.0164	EADFIKKMY	9	9.348	1000000.0	113941.0	1000000.0
PIR2	T28161		917	98.0165	ATICRAMKY	9	5.412	1000000.0	112.4	1000000.0
PIR2	T28161		1192	98.0033	KTDEQYNENY	10	5.386	1000000.0	1911.8	1000000.0
PIR2	T28161		1201	98.0034	YTFKNPPPQY	10	8.064	1000000.0	918.8	1000000.0
PIR2	T28161		1884	98.0166	WLEYFLDDY	9	8.602	1000000.0	35096.0	1000000.0
PIR2	T28161		2221	98.0167	ITSSSESEY	9	9.299	1000000.0	1168.0	1000000.0
55.t00004	Chromosome14		45	98.0168	YVDIGSNIY	9	3.352	1000000.0	18704.2	1000000.0
55.t00004	Chromosome14		457	98.0169	DTCKNIWNY	9	3.842	1000000.0	878.3	1000000.0
55.t00004	Chromosome14		563	98.0170	LSQGKKNTY	9	10.561	1000000.0	40514.9	1000000.0
55.t00004	Chromosome14		928	98.0171	NIDCVISPY	9	8.449	1000000.0	3464.1	1000000.0

Table 2:
Pf-derived A1 supertype peptides with PIC <20nM

Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	PIC A*0101 PIC	A*0201	A*1101	PIC A*2402 PIC
55.t00004	Chromosome14		953	98.0172	NMDNLLFTY	9	5.144	1000000.0	413.3	6464.5
55.t00004	Chromosome14		1105	98.0035	FVDHNYNYNY	10	6.601	1000000.0	687.9	1000000.0
55.t00004	Chromosome14		1261	98.0173	HSKENQQKY	9	3.798	1000000.0	41445.3	1000000.0
55.t00004	Chromosome14		1339	98.0174	VSEGYTSTY	9	7.735	1000000.0	4760.1	1000000.0
55.t00004	Chromosome14		1358	98.0175	FMDSQNGMY	9	8.455	1000000.0	21913.6	2720.6
55.t00004	Chromosome14		1537	98.0036	NSYNDSLINY	10	12.536	1000000.0	1846.9	1000000.0
13.t00011	Chromosome14		27	98.0176	STGINEENY	9	6.590	1000000.0	838.9	1000000.0
13.t00011	Chromosome14		44	98.0177	MNETVFLDY	9	5.456	1000000.0	1000000.0	1000000.0
13.t00011	Chromosome14		77	98.0178	LTSKVWDTY	9	6.496	1000000.0	616.6	1000000.0
37.t00002	Chromosome14		10	98.0179	KHDALTYMY	9	23.541	1000000.0	1000000.0	1000000.0
37.t00002	Chromosome14		14	98.0180	LTYMYCVYY	9	10.044	1000000.0	20.3	1000000.0
674.t00001	Chromosome11		201	98.0181	NIDINDLGY	9	10.069	1000000.0	23874.2	1000000.0
674.t00001	Chromosome11		260	98.0182	ISSNQFNNY	9	6.099	1000000.0	2575.9	1000000.0
674.t00001	Chromosome11		400	98.0183	DIEPLISSY	9	14.646	1000000.0	183727.1	1000000.0
674.t00001	Chromosome11		453	98.0037	VTNNDSINNY	10	17.920	1000000.0	1310.7	1000000.0
674.t00001	Chromosome11		772	98.0184	ESGKNMEHY	9	8.198	1000000.0	75390.5	1000000.0
674.t00001	Chromosome11		868	98.0185	LKDFDMLLY	9	12.047	1000000.0	1000000.0	1000000.0
674.t00001	Chromosome11		936	98.0186	YIDVEDDDY	9	13.870	1000000.0	377275.0	1000000.0
674.t00001	Chromosome11		1001	98.0187	DMDDNYYLY	9	3.056	1000000.0	2478.6	45380.9
674.t00001	Chromosome11		1224	98.0188	YGDNNKDCY	9	19.772	1000000.0	368191.0	1000000.0
674.t00001	Chromosome11		1239	98.0189	IYDFNNNSY	9	17.735	1000000.0	1000000.0	365.4

Table 3:
Pf-derived A24 supertype peptides with PIC <100nM

							PIC			
Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	A*0101 PIC	A*0201	A*1101	A*2402 PIC
331.t00003	Chromosome10		10	98.0206	FYKKKRNVL	9	67134.0	1000000.0	1000000.0	1.708
331.t00003	Chromosome10		110	98.0207	VYEINKNEF	9	84.1	1000000.0	1000000.0	2.011
331.t00003	Chromosome10		604	98.0208	FFVWGHDMF	9	221.0	1000000.0	1000000.0	3.642
331.t00003	Chromosome10		684	98.0209	VYNIKENFW	9	123239.4	1000000.0	1000000.0	2.687
331.t00003	Chromosome10		1108	98.0210	KYNLCHNML	9	147073.6	1000000.0	1000000.0	0.324
331.t00003	Chromosome10		1268	98.0211	FYVPIKKKL	9	172677.3	1000000.0	1000000.0	2.705
331.t00003	Chromosome10		1365	98.0212	KYEIIGNIL	9	89209.4	1000000.0	1000000.0	1.961
331.t00003	Chromosome10		1449	98.0213	FWLAIKDIF	9	173.9	1000000.0	1000000.0	1.093
331.t00003	Chromosome10		1515	98.0214	LYRRRKNLF	9	113.5	1000000.0	1000000.0	1.220
331.t00003	Chromosome10		1704	98.0215	IYIIKQNSF	9	111.6	1000000.0	1000000.0	0.256
18.000811	Chr12Contig18		5	98.0190	LFVCFLIFHF	10	672.3	1000000.0	1000000.0	19.783
18.000811	Chr12Contig18		8	98.0191	CFLIFHFFLF	10	1385.7	1000000.0	1000000.0	18.444
18.000811	Chr12Contig18		8	98.0216	CFLIFHFFL	9	106491.6	1000000.0	1000000.0	0.321
18.000811	Chr12Contig18		11	98.0217	IFHFFLFLL	9	53306.2	1000000.0	1000000.0	38.527
18.000811	Chr12Contig18		13	98.0192	HFFLFLLYIL	10	1000000.0	1000000.0	1000000.0	35.659
18.000811	Chr12Contig18		13	98.0218	HFFLFLLYI	9	24845.8	1000000.0	1000000.0	26.159
18.000811	Chr12Contig18		14	98.0219	FFLFLLYIL	9	62569.1	1000000.0	1000000.0	32.471
18.000811	Chr12Contig18		19	98.0220	LYILFLVKM	9	90645.8	1000000.0	1000000.0	63.051
18.000811	Chr12Contig18		41	98.0221	VFLVFSNVL	9	178682.3	1000000.0	1000000.0	5.555
18.000811	Chr12Contig18		160	98.0222	TYGIIVPVL	9	123562.9	1000000.0	1000000.0	3.015
MY924Fe3.pltl			153	98.0223	FFNVFNIFF	9	45.6	1000000.0	1000000.0	0.470
MY924Fe3.pltl			1412	98.0224	FYSWLQNVL	9	83170.3	1000000.0	1000000.0	2.428
MY924Fe3.pltl			1435	98.0225	FYERFSDLI	9	46149.1	1000000.0	1000000.0	0.625
MY924Fe3.pltl			1534	98.0226	VYLIQNNYI	9	615175.4	1000000.0	1000000.0	0.632
MY924Fe3.pltl			1557	98.0227	NYMKNSFYI	9	24802.7	1000000.0	1000000.0	2.200
MY924Fe3.pltl			1800	98.0228	VYCNYVTEI	9	160654.7	1000000.0	1000000.0	3.071

Table 3:
Pf-derived A24 supertype peptides with PIC <100nM

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	A*0101 PIC	A*0201	A*1101	A*2402 PIC
MY924Fe3.pltl			1839	98.0229	HYEVLPYKF	9	14.6	1000000.0	1000000.0	2.621
MY924Fe3.pltl			1846	98.0230	KFTIIVESL	9	181796.5	1000000.0	1000000.0	1.946
MY924Fe3.pltl			2159	98.0231	FMTRAHFHI	9	9020.6	52.2	1000000.0	1.455
MY924Fe3.pltl			2380	98.0232	FYKSKVIII	9	53263.7	1000000.0	1000000.0	0.928
MP03001	MAL3P2.11	CAB38998	11	98.0233	SFLFVEALF	9	80.3	1000000.0	1000000.0	53.045
MP03001	MAL3P2.11	CAB38998	54	98.0234	YYGKQENWY	9	73.1	1000000.0	1000000.0	49.750
MP03001	MAL3P2.11	CAB38998	369	98.0235	KMEKCSSVF	9	34.0	1000000.0	1000000.0	39.989
MP03001	MAL3P2.11	CAB38998	376	98.0236	VFNVVNSSI	9	231723.3	1000000.0	1000000.0	82.506
1369.t00001	Chromosome 11		34	98.0237	NYMKIMNHL	9	37582.2	1000000.0	1000000.0	4.875
1369.t00001	Chromosome 11		225	98.0193	SYKSSKRDKF	10	1632.7	1000000.0	1000000.0	46.746
1369.t00001	Chromosome 11		264	98.0238	TYKKKNNHI	9	90904.7	1000000.0	1000000.0	12.042
1369.t00001	Chromosome 11		277	98.0239	VYYNILIVL	9	59837.4	1000000.0	1000000.0	11.637
1369.t00001	Chromosome 11		285	98.0240	LYYLFNQHI	9	56431.2	1000000.0	1000000.0	5.598
1369.t00001	Chromosome 11		310	98.0241	SFFMNRFYI	9	56480.3	1000000.0	1000000.0	80.940
1369.t00001	Chromosome 11		316	98.0242	FYITTRYKY	9	45.2	1000000.0	1000000.0	3.968
1369.t00001	Chromosome 11		328	98.0243	KYINFINFI	9	289163.4	1000000.0	1000000.0	0.095
1369.t00001	Chromosome 11		331	98.0244	NFINFIKVL	9	610070.5	1000000.0	1000000.0	37.188
1369.t00001	Chromosome 11		380	98.0245	KYEALIKLL	9	105887.8	1000000.0	1000000.0	9.605
699.t00001	Chromosome 11		443	98.0246	FFFSLIDYF	9	118.9	1000000.0	1000000.0	1.331
699.t00001	Chromosome 11		460	98.0247	KYNIKVCEL	9	98354.1	1000000.0	1000000.0	0.429
699.t00001	Chromosome 11		487	98.0248	FYLYISFLL	9	34312.8	1000000.0	1000000.0	0.417
699.t00001	Chromosome 11		664	98.0249	FYTNNANLL	9	42910.8	1000000.0	1000000.0	0.639
699.t00001	Chromosome 11		766	98.0250	EYNPSFFYL	9	22929.4	1000000.0	1000000.0	1.772
699.t00001	Chromosome 11		845	98.0251	SFIIFKNIF	9	249.9	1000000.0	1000000.0	3.449
699.t00001	Chromosome 11		881	98.0252	LYMNFLKFI	9	34148.2	1000000.0	1000000.0	4.363
699.t00001	Chromosome 11		929	98.0253	KYLIILLYI	9	93640.1	1000000.0	1000000.0	1.034

Table 3:
Pf-derived A24 supertype peptides with PIC <100nM

							PIC			
Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	A*0101 PIC	A*0201	A*1101	A*2402 PIC
699.t00001	Chromosome 11		1020	98.0254	KYIYIYIYI	9	215740.5	1000000.0	1000000.0	0.296
699.t00001	Chromosome 11		1024	98.0255	IYIYIFIYL	9	52331.1	1000000.0	1000000.0	2.300
M13Hg2.q1t3			135	98.0256	IYINKLSFF	9	67.4	1000000.0	1000000.0	3.329
M13Hg2.q1t3			142	98.0257	FFSIKDELF	9	27.2	1000000.0	1000000.0	14.276
M13Hg2.q1t3			156	98.0258	EFLKNNSYF	9	164.9	1000000.0	1000000.0	20.204
M13Hg2.q1t3			163	98.0259	YFNIIQQKI	9	45274.1	1000000.0	1000000.0	13.888
M13Hg2.q1t3			244	98.0260	WYCSACNFL	9	56993.5	1000000.0	1000000.0	7.339
M13Hg2.q1t3			296	98.0261	LYLINNKNL	9	150801.1	1000000.0	1000000.0	28.854
M13Hg2.q1t3			345	98.0262	TYKDANNNI	9	71978.1	1000000.0	1000000.0	29.035
M13Hg2.q1t3			521	98.0263	VYEKEKQYF	9	103.6	1000000.0	1000000.0	3.963
M13Hg2.q1t3			553	98.0194	PYFNFFVNYF	10	185.8	1000000.0	1000000.0	33.503
M13Hg2.q1t3			889	98.0264	IYNNNNEHI	9	77962.6	1000000.0	1000000.0	24.919
Mal_5L10c4.q1t6			78	98.0265	EYNKYNEYF	9	90.4	1000000.0	1000000.0	3.130
Mal_5L10c4.q1t6			137	98.0266	NYVNNNNVF	9	220.5	1000000.0	1000000.0	3.441
Mal_5L10c4.q1t6			321	98.0267	KYPIKYCEL	9	183114.8	1000000.0	1000000.0	0.364
Mal_5L10c4.q1t6			416	98.0268	AYHDLIKLF	9	66.8	1000000.0	1000000.0	4.671
Mal_5L10c4.q1t6			533	98.0269	KYISSVNYF	9	194.8	1000000.0	1000000.0	0.018
Mal_5L10c4.q1t6			773	98.0270	KYDWFFNSF	9	34.0	1000000.0	1000000.0	0.374
Mal_5L10c4.q1t6			1183	98.0271	HYVIKKYII	9	133499.1	1000000.0	1000000.0	1.507
Mal_5L10c4.q1t6			1259	98.0272	LYLHIHKLF	9	72.0	1000000.0	1000000.0	0.343
Mal_5L10c4.q1t6			1323	98.0273	YYRTNYGYI	9	165642.6	1000000.0	1000000.0	4.072
Mal_5L10c4.q1t6			2054	98.0274	KYLRYHSQL	9	421667.1	1000000.0	1000000.0	0.655
571.t00003	Chromosome11		74	98.0275	FYIDKCIHF	9	23.2	1000000.0	1000000.0	0.120
571.t00003	Chromosome11		162	98.0276	FYTNYYQSF	9	48.3	1000000.0	1000000.0	0.186
571.t00003	Chromosome11		177	98.0277	PYINQTNIF	9	228.9	1000000.0	1000000.0	0.527
571.t00003	Chromosome11		807	98.0278	NYPNNANHI	9	176667.0	1000000.0	1000000.0	3.103

Table 3:
Pf-derived A24 supertype peptides with PIC <100nM

							PIC			
Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	A*0101 PIC	A*0201	A*1101	A*2402 PIC
571.t00003	Chromosome11		834	98.0279	TYNNFHNSY	9	52.4	1000000.0	1000000.0	0.776
571.t00003	Chromosome11		1917	98.0280	YMNNNTYSF	9	7.7	1000000.0	1000000.0	2.132
571.t00003	Chromosome11		2026	98.0281	KYTEGATNF	9	74.8	1000000.0	1000000.0	1.964
571.t00003	Chromosome11		2450	98.0282	FYISIIDII	9	150563.0	1000000.0	1000000.0	1.632
571.t00003	Chromosome11		2540	98.0283	YYKEHISEF	9	96.3	1000000.0	1000000.0	3.143
571.t00003	Chromosome11		2914	98.0284	YYNRANNEI	9	46291.4	1000000.0	1000000.0	3.342
MP03072	PFC0450w	CAA15614	17	98.0285	AFLLITFLM	9	37258.4	1000000.0	1000000.0	17.525
MP03072	PFC0450w	CAA15614	53	98.0195	LYVIFLVLLF	10	174.0	1000000.0	1000000.0	16.581
MP03072	PFC0450w	CAA15614	53	98.0286	LYVIFLVLL	9	107336.6	1000000.0	1000000.0	5.089
MP03072	PFC0450w	CAA15614	86	98.0287	KYVQLASTY	9	65.1	1000000.0	1000000.0	70.547
45.t00001	Chromosome14		21	98.0196	RYQDPQNYEL	10	1000000.0	1000000.0	1000000.0	46.471
45.t00001	Chromosome14		40	98.0288	IYYFDGNSW	9	97026.0	1000000.0	1000000.0	15.493
45.t00001	Chromosome14		94	98.0289	VYRHCEYIL	9	560574.8	1000000.0	1000000.0	27.538
45.t00001	Chromosome14		135	98.0290	TWKPTIFLL	9	34068.5	1000000.0	1000000.0	26.741
45.t00001	Chromosome14		168	98.0291	SYKVNCINF	9	25.3	1000000.0	1000000.0	63.592
45.t00001	Chromosome14		216	98.0292	KYNYFIHFF	9	39.1	1000000.0	1000000.0	0.380
45.t00001	Chromosome14		218	98.0293	NYFIHFFTW	9	95820.5	1000000.0	1000000.0	2.156
45.t00001	Chromosome14		222	98.0294	HFFTWGTMF	9	17.4	1000000.0	1000000.0	6.418
45.t00001	Chromosome14		229	98.0295	MFVPKYFEL	9	57423.3	1000000.0	1000000.0	28.589
45.t00001	Chromosome14		295	98.0296	IYTIIQDQL	9	334935.0	1000000.0	1000000.0	9.774
MP03137	PFC0700c	CAB11150	3	98.0197	DFFLKSKFNI	10	1000000.0	1000000.0	1000000.0	79.527
MP03137	PFC0700c	CAB11150	4	98.0297	FFLKSKFNI	9	80470.7	1000000.0	1000000.0	10.043
MP03137	PFC0700c	CAB11150	9	98.0298	KFNILSSPL	9	275819.0	1000000.0	1000000.0	48.661
MP03137	PFC0700c	CAB11150	61	98.0299	RMTSLKNEL	9	45471.5	1089.6	1000000.0	50.292
MP03137	PFC0700c	CAB11150	77	98.0300	YYNNFNNNY	9	29.9	1000000.0	1000000.0	2.802
MP03137	PFC0700c	CAB11150	87	98.0301	YYNKSTEKL	9	25069.1	1000000.0	1000000.0	6.131

Table 3:
Pf-derived A24 supertype peptides with PIC <100nM

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	A*0101 PIC	A*0201	A*1101	A*2402 PIC
MP03137	PFC0700c	CAB11150	109	98.0302	EYEPTANLL	9	29899.8	1000000.0	1000000.0	9.359
12.t00018	Chromosome14		479	98.0303	PYEEVENYF	9	118.2	1000000.0	1000000.0	3.525
12.t00018	Chromosome14		506	98.0304	KFILHMTLL	9	418744.3	1000000.0	1000000.0	7.942
12.t00018	Chromosome14		544	98.0305	NFLNIYASL	9	309896.9	1000000.0	1000000.0	7.653
12.t00018	Chromosome14		594	98.0306	VWKKLIEYF	9	120.2	1000000.0	1000000.0	7.058
12.t00018	Chromosome14		614	98.0307	LYVSMYIPF	9	113.5	1000000.0	1000000.0	6.679
12.t00018	Chromosome14		618	98.0308	MYIPFIKKF	9	62.3	1000000.0	1000000.0	2.663
12.t00018	Chromosome14		625	98.0309	KFYDKRFIF	9	53.3	1000000.0	1000000.0	1.395
12.t00018	Chromosome14		675	98.0310	IYNMYHNNF	9	27.2	1000000.0	1000000.0	0.737
12.t00018	Chromosome14		678	98.0311	MYHNNFSYF	9	61.8	1000000.0	1000000.0	5.105
12.t00018	Chromosome14		815	98.0312	KYDITKNLI	9	86746.4	1000000.0	1000000.0	2.983
mal_BU121g9.q1c1			61	98.0313	GYFKRIFKL	9	39278.5	1000000.0	1000000.0	64.889
mal_BU121g9.q1c1			81	98.0314	TYKNGNIYI	9	240142.1	1000000.0	1000000.0	20.110
mal_BU121g9.q1c1			87	98.0315	IYIYIYIYI	9	133656.3	1000000.0	1000000.0	2.246
mal_BU121g9.q1c1			89	98.0198	IYIYIYIYFL	10	1000000.0	1000000.0	1000000.0	72.026
mal_BU121g9.q1c1			89	98.0316	IYIYIYIYF	9	89.8	1000000.0	1000000.0	0.543
mal_9A57b11.q1t2			75	98.0317	IFKNDNNTF	9	290.7	1000000.0	1000000.0	11.568
mal_9A57b11.q1t2			103	98.0318	KYGNICHHI	9	61693.1	1000000.0	1000000.0	4.552
mal_9A57b11.q1t2			139	98.0319	QYTDIPSLI	9	41835.9	1000000.0	1000000.0	24.727
mal_9A57b11.q1t2			159	98.0320	VFCYEYFIF	9	98.9	1000000.0	1000000.0	69.226
mal_9A57b11.q1t2			161	98.0199	CYEYFIFDIF	10	811.1	1000000.0	1000000.0	61.974
mal_9A57b11.q1t2			161	98.0321	CYEYFIFDI	9	32300.1	1000000.0	1000000.0	79.659
mal_9A57b11.q1t2			171	98.0322	KYARNILSL	9	27927.9	1000000.0	1000000.0	3.398
mal_9A57b11.q1t2			230	98.0323	IFVKYLPLF	9	68.2	1000000.0	1000000.0	30.518
mal_9A57b11.q1t2			233	98.0324	KYLPLFLMM	9	16925.5	1000000.0	1000000.0	15.776
mal_9A57b11.q1t2			237	98.0325	LFLMMEHSF	9	51.0	1000000.0	1000000.0	70.804

Table 3:
Pf-derived A24 supertype peptides with PIC <100nM

							PIC			
Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	A*0101 PIC	A*0201	A*1101	A*2402 PIC
mal_BL50e8.plca_5			116	98.0326	QYSNYFDYL	9	103941.7	1000000.0	1000000.0	17.499
mal_BL50e8.plca_5			184	98.0327	PYETNNNLF	9	37.2	1000000.0	1000000.0	4.367
mal_BL50e8.plca_5			341	98.0328	YYSRRVEKI	9	33168.4	1000000.0	1000000.0	6.349
mal_BL50e8.plca_5			555	98.0329	KFKWIQDNL	9	453346.6	1000000.0	1000000.0	30.007
mal_BL50e8.plca_5			687	98.0200	RYVGLGSFHF	10	1143.3	1000000.0	1000000.0	33.267
mal_BL50e8.plca_5			768	98.0330	TYKMYPPEF	9	68.2	1000000.0	1000000.0	7.746
mal_BL50e8.plca_5			771	98.0331	MYPPEFNTL	9	37286.8	1000000.0	1000000.0	14.291
mal_BL50e8.plca_5			827	98.0332	KYCIGSTYF	9	184.3	1000000.0	1000000.0	0.261
mal_BL50e8.plca_5			833	98.0333	TYFLRQVSI	9	163553.3	1000000.0	1000000.0	31.623
mal_BL50e8.plca_5			857	98.0334	KYSARLHPI	9	52609.1	1000000.0	1000000.0	33.171
M13S8h6.plt_3			152	98.0335	FYLKKKFLF	9	30.5	1000000.0	1000000.0	0.091
M13S8h6.plt_3			298	98.0336	KYYISYKVL	9	328554.4	1000000.0	1000000.0	3.468
M13S8h6.plt_3			321	98.0337	KYINKNISL	9	213679.4	1000000.0	1000000.0	0.395
M13S8h6.plt_3			380	98.0338	KYLKEDNTF	9	189.5	1000000.0	1000000.0	2.580
M13S8h6.plt_3			753	98.0339	KYGDNENNF	9	50.4	1000000.0	1000000.0	2.048
M13S8h6.plt_3			1208	98.0340	VFTKINNLF	9	55.7	1000000.0	1000000.0	4.101
M13S8h6.plt_3			1438	98.0341	IWLIRSIYL	9	175087.7	1000000.0	1000000.0	2.659
M13S8h6.plt_3			1444	98.0342	IYLFIITYI	9	153399.4	1000000.0	1000000.0	4.385
M13S8h6.plt_3			1536	98.0343	FFFVFFYIF	9	26.2	1000000.0	1000000.0	0.631
M13S8h6.plt_3			1541	98.0344	FYIFLIYSF	9	60.5	1000000.0	1000000.0	0.315
585.t00002	Chromosome11		1	98.0345	MYIFFFILF	9	12.6	1000000.0	1000000.0	1.911
585.t00002	Chromosome11		11	98.0346	FYVMSTYTF	9	45.7	1000000.0	1000000.0	0.144
585.t00002	Chromosome11		512	98.0347	RYCTKCFLW	9	31357.1	1000000.0	1000000.0	1.726
585.t00002	Chromosome11		605	98.0348	VYAKNIPLW	9	36459.4	1000000.0	1000000.0	1.882
585.t00002	Chromosome11		663	98.0349	FFCIFFISL	9	35177.1	1000000.0	1000000.0	1.436
585.t00002	Chromosome11		681	98.0350	PYYKKKNLF	9	53.3	1000000.0	1000000.0	2.732

Table 3:
Pf-derived A24 supertype peptides with PIC <100nM

							PIC			
Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	A*0101 PIC	A*0201	A*1101	A*2402 PIC
585.t00002	Chromosome11		1378	98.0351	FYTLVNILI	9	40959.2	1000000.0	1000000.0	2.113
585.t00002	Chromosome11		1419	98.0352	YFIIRSYEL	9	135598.6	1000000.0	1000000.0	2.721
585.t00002	Chromosome11		1483	98.0353	KYICLTCAF	9	30.1	1000000.0	1000000.0	0.435
585.t00002	Chromosome11		1752	98.0354	KYDLFNNFI	9	83062.5	1000000.0	1000000.0	1.355
1223.t00015	mal_9A21f9.q1t_4		1202	98.0355	KYKDMAKIF	9	215.2	1000000.0	1000000.0	0.315
1223.t00015	mal_9A21f9.q1t_4		1599	98.0356	GYRPFIYSW	9	83421.5	1000000.0	1000000.0	3.292
1223.t00015	mal_9A21f9.q1t_4		1621	98.0357	LYAIFNKLF	9	57.9	1000000.0	1000000.0	0.212
1223.t00015	mal_9A21f9.q1t_4		1631	98.0358	FYLDKIQIL	9	36632.3	1000000.0	1000000.0	0.942
1223.t00015	mal_9A21f9.q1t_4		2272	98.0359	RMEDKTFSL	9	8870.6	143.4	1000000.0	4.349
1223.t00015	mal_9A21f9.q1t_4		2702	98.0360	IYNCVTINW	9	10684.6	1000000.0	1000000.0	2.727
1223.t00015	mal_9A21f9.q1t_4		3109	98.0361	RWTDDSNNF	9	60.4	1000000.0	1000000.0	1.600
1223.t00015	mal_9A21f9.q1t_4		3735	98.0362	FFYDILNVI	9	40209.1	1000000.0	1000000.0	5.095
1223.t00015	mal_9A21f9.q1t_4		3968	98.0363	KYRKIIYSL	9	215862.1	1000000.0	1000000.0	0.665
1223.t00015	mal_9A21f9.q1t_4		4515	98.0364	KYFIFRIHL	9	114989.5	1000000.0	1000000.0	0.325
599.t00001	Chromosome11		8	98.0365	KYLTINFFI	9	160943.0	1000000.0	1000000.0	0.123
599.t00001	Chromosome11		14	98.0366	FFILLTLVF	9	30.5	1000000.0	1000000.0	3.495
599.t00001	Chromosome11		24	98.0367	KYSSCQNSL	9	213208.8	1000000.0	1000000.0	0.906
599.t00001	Chromosome11		955	98.0368	KFIEHINEF	9	278.8	1000000.0	1000000.0	1.175
599.t00001	Chromosome11		1118	98.0369	KYIELNDLI	9	231736.4	1000000.0	1000000.0	1.464
599.t00001	Chromosome11		1194	98.0370	PYSNVTYVI	9	97127.6	1000000.0	1000000.0	1.861
599.t00001	Chromosome11		1434	98.0371	MYDILNAYF	9	42.0	1000000.0	1000000.0	1.204
599.t00001	Chromosome11		1769	98.0372	HYIMNNTIF	9	38.3	1000000.0	1000000.0	1.389
599.t00001	Chromosome11		1929	98.0373	FFKYIISYF	9	126.1	1000000.0	1000000.0	3.000
599.t00001	Chromosome11		1943	98.0374	KYLNDDNYL	9	679247.8	1000000.0	1000000.0	0.368
MP01072	M1045c5.p1c.C_6		67	98.0375	LYKSIFKAF	9	52.5	1000000.0	1000000.0	21.749
MP01072	M1045c5.p1c.C_6		107	98.0376	SYRIVNAGF	9	268.7	1000000.0	1000000.0	7.480

Table 3:
Pf-derived A24 supertype peptides with PIC <100nM

							PIC			
Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	A*0101 PIC	A*0201	A*1101	A*2402 PIC
MP01072	M1045c5.plc.C_6		319	98.0377	KYTFRSLSI	9	63496.4	1000000.0	1000000.0	7.958
MP01072	M1045c5.plc.C_6		388	98.0378	KYKNDSNRI	9	401700.0	1000000.0	1000000.0	6.170
MP01072	M1045c5.plc.C_6		612	98.0379	SYIYNKNIF	9	105.6	1000000.0	1000000.0	13.043
MP01072	M1045c5.plc.C_6		1042	98.0380	FMKNNTTLF	9	11.7	1000000.0	1000000.0	2.141
MP01072	M1045c5.plc.C_6		1123	98.0381	HYVMINNNL	9	52910.4	1000000.0	1000000.0	3.607
MP01072	M1045c5.plc.C_6		1163	98.0382	FFLFFSIFI	9	69264.3	1000000.0	1000000.0	2.646
MP01072	M1045c5.plc.C_6		1249	98.0383	RYFLHTITI	9	101443.4	1000000.0	1000000.0	2.834
MP01072	M1045c5.plc.C_6		1260	98.0384	KYTSSYDSL	9	230897.9	1000000.0	1000000.0	1.533
PIR2	T28161		243	98.0385	YYKLREDWW	9	283854.6	1000000.0	1000000.0	8.617
PIR2	T28161		304	98.0386	QYLRWFEEW	9	35188.7	1000000.0	1000000.0	14.859
PIR2	T28161		628	98.0387	HWTQIKKHF	9	30.8	1000000.0	1000000.0	11.497
PIR2	T28161		647	98.0388	HYFVLETVL	9	65432.8	1000000.0	1000000.0	12.976
PIR2	T28161		833	98.0389	RWMDTAGFI	9	32693.4	1000000.0	1000000.0	6.822
PIR2	T28161		848	98.0201	IYMPPRRQHF	10	391.2	1000000.0	1000000.0	14.666
PIR2	T28161		1024	98.0390	RWMTEWAEW	9	39609.0	1000000.0	1000000.0	3.877
PIR2	T28161		1574	98.0391	KYQYDKVKL	9	515925.0	1000000.0	1000000.0	6.877
PIR2	T28161		1681	98.0392	KYCRFYKRW	9	239673.9	1000000.0	1000000.0	3.433
PIR2	T28161		1887	98.0393	YFLDDYNKI	9	114991.6	1000000.0	1000000.0	7.588
55.t00004	Chromosome14		223	98.0394	KYELRKTSI	9	226076.9	1000000.0	1000000.0	3.213
55.t00004	Chromosome14		339	98.0395	MYKNKVDPL	9	208222.7	1000000.0	1000000.0	31.490
55.t00004	Chromosome14		455	98.0396	YYDTCKNIW	9	80910.8	1000000.0	1000000.0	11.820
55.t00004	Chromosome14		686	98.0397	KYINNMSFI	9	317672.0	1000000.0	1000000.0	1.757
55.t00004	Chromosome14		896	98.0398	LYPWKENKF	9	99.5	1000000.0	1000000.0	6.128
55.t00004	Chromosome14		973	98.0399	KWNVFNNSI	9	191824.8	1000000.0	1000000.0	0.536
55.t00004	Chromosome14		1027	98.0400	KFKIINSYI	9	648818.6	1000000.0	1000000.0	2.246
55.t00004	Chromosome14		1123	98.0401	NYAYDNIEL	9	113781.7	1000000.0	1000000.0	8.937

Table 3:
Pf-derived A24 supertype peptides with PIC <100nM

							PIC			
Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	A*0101 PIC	A*0201	A*1101	A*2402 PIC
55.t00004	Chromosome14		1155	98.0402	IYTSTNNII	9	105468.3	1000000.0	1000000.0	7.723
55.t00004	Chromosome14		1268	98.0403	KYTYNINNL	9	65476.9	1000000.0	1000000.0	7.681
13.t00011	Chromosome14		68	98.0202	RYNVINHIYL	10	1000000.0	1000000.0	1000000.0	74.419
13.t00011	Chromosome14		68	98.0404	RYNVINHIY	9	26.0	1000000.0	1000000.0	55.779
13.t00011	Chromosome14		84	98.0405	TYNYLTPTL	9	75416.9	1000000.0	1000000.0	7.874
13.t00011	Chromosome14		96	98.0203	RFRVFKDYSF	10	3387.1	1000000.0	1000000.0	29.344
13.t00011	Chromosome14		99	98.0406	VFKDYSFFI	9	99598.3	1000000.0	1000000.0	7.373
13.t00011	Chromosome14		105	98.0407	FFIDEVKKI	9	230004.2	1000000.0	1000000.0	12.686
37.t00002	Chromosome14		20	98.0408	VYYDNYESL	9	72350.5	1000000.0	1000000.0	10.652
674.t00001	Chromosome11		68	98.0409	RFVEKIYYL	9	228887.0	1000000.0	1000000.0	8.045
674.t00001	Chromosome11		114	98.0410	IYINVQKNL	9	306183.0	1000000.0	1000000.0	14.033
674.t00001	Chromosome11		140	98.0411	KFYYYFKEF	9	92.8	1000000.0	1000000.0	14.487
674.t00001	Chromosome11		141	98.0204	FYYYFKEFLL	10	1000000.0	1000000.0	1000000.0	13.628
674.t00001	Chromosome11		141	98.0412	FYYYFKEFL	9	104311.6	1000000.0	1000000.0	1.300
674.t00001	Chromosome11		418	98.0413	TYIPDKKLL	9	209801.1	1000000.0	1000000.0	17.181
674.t00001	Chromosome11		461	98.0414	NYLYNKYYI	9	288938.1	1000000.0	1000000.0	5.750
674.t00001	Chromosome11		579	98.0415	NFKEQHLLF	9	72.4	1000000.0	1000000.0	38.780
674.t00001	Chromosome11		649	98.0416	HYINNKHNL	9	41447.1	1000000.0	1000000.0	10.887
674.t00001	Chromosome11		800	98.0417	LYREHSREL	9	274526.6	1000000.0	1000000.0	38.601
674.t00001	Chromosome11		1095	98.0418	NYINNNIYL	9	268777.1	1000000.0	1000000.0	3.259
674.t00001	Chromosome11		1117	98.0419	NYNQKENSF	9	40.2	1000000.0	1000000.0	27.868
674.t00001	Chromosome11		1396	98.0205	QYKVKIKPVF	10	5076.8	1000000.0	1000000.0	42.788

Table 4:
Pf-derived A2 supertype peptides with PIC <100nM

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101	A*2402
331.t00003	Chromosome10	105		99.0042	LIYPCVYEI	9	38050.5	43.8	1000000.0	1000000.0
331.t00003	Chromosome10	598		99.0043	NMNVQNFFV	9	50979.5	35.3	1000000.0	1000000.0
331.t00003	Chromosome10	605		99.0044	FVWGHDMFM	9	25516.6	18.5	1000000.0	1000000.0
331.t00003	Chromosome10	660		99.0045	QLDDKFAFI	9	3138.5	43.0	1000000.0	1000000.0
331.t00003	Chromosome10	950		99.0046	CLINHNFFM	9	63467.3	65.7	1000000.0	1000000.0
331.t00003	Chromosome10	957		99.0047	FMLVGGINI	9	11445.4	72.5	1000000.0	399.0
331.t00003	Chromosome10	1007		99.0048	YIIGGGCTV	9	19833.9	77.9	1000000.0	1000000.0
331.t00003	Chromosome10	1016		99.0049	FTFGSFFDV	9	2705.2	14.1	1000000.0	1000000.0
331.t00003	Chromosome10	1847		99.0050	NLSFAQYTL	9	22775.6	52.7	1000000.0	1000000.0
331.t00003	Chromosome10	1889		99.0051	RMYHYVVDI	9	47589.4	49.4	1000000.0	890.2
18.000811	Chr12Contig18	2		99.0001	VLRLFVCFLI	10	1000000.0	72.4	1000000.0	1000000.0
18.000811	Chr12Contig18	9		99.0002	FLIFHFFLFL	10	1000000.0	10.9	1000000.0	1000000.0
18.000811	Chr12Contig18	10		99.0003	LIFHFFLFLL	10	1000000.0	29.1	1000000.0	1000000.0
18.000811	Chr12Contig18	15		99.0004	FLFLLYILFL	10	404264.4	19.6	1000000.0	1000000.0
18.000811	Chr12Contig18	32		99.0005	RLPVICSFLV	10	1000000.0	99.3	1000000.0	1000000.0
18.000811	Chr12Contig18	35		99.0006	VICSFLVFLV	10	1000000.0	71.5	1000000.0	1000000.0
18.000811	Chr12Contig18	39		99.0007	FLVFLVFSNV	10	1000000.0	45.6	1000000.0	1000000.0
18.000811	Chr12Contig18	10		99.0052	LIFHFFLFL	9	8592.7	9.8	1000000.0	1000000.0
18.000811	Chr12Contig18	17		99.0053	FLLYILFLV	9	6742.1	1.9	1000000.0	1000000.0
18.000811	Chr12Contig18	35		99.0054	VICSFLVFL	9	43080.6	76.0	1000000.0	1000000.0
18.000811	Chr12Contig18	159		99.0055	ATYGIIVPV	9	18077.0	45.4	1000000.0	1000000.0
MY924Fe3.p1t1		222		99.0008	FLYAFNKYYV	10	538964.2	15.2	1000000.0	1000000.0
MY924Fe3.p1t1		127		99.0056	NMISVVYYI	9	97099.2	14.5	1000000.0	8.2
MY924Fe3.p1t1		299		99.0057	SLCFYFLLL	9	2719.7	20.9	1000000.0	1000000.0
MY924Fe3.p1t1		470		99.0058	ILFLHNYLL	9	31359.3	26.7	1000000.0	1000000.0
MY924Fe3.p1t1		512		99.0059	YLDVYNFLL	9	4353.0	7.2	1000000.0	1000000.0
MY924Fe3.p1t1		1209		99.0060	FQLYYMYYL	9	91212.8	4.0	1000000.0	1000000.0
MY924Fe3.p1t1		1267		99.0061	YVMDKVLRL	9	984.8	45.3	1000000.0	1000000.0

Table 4:
Pf-derived A2 supertype peptides with PIC <100nM

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101	A*2402
MY924Fe3.p1t1		2260		99.0062	LLFILSHFI	9	11073.4	23.7	1000000.0	1000000.0
MY924Fe3.p1t1		2326		99.0063	YLVNYCLVV	9	16842.3	10.9	1000000.0	1000000.0
MY924Fe3.p1t1		2395		99.0064	KIYVCIYYL	9	157982.7	39.3	1000000.0	1000000.0
MP03001	MAL3P2.11	6	CAB38998	99.0009	ILSVSSFLFV	10	1000000.0	94.9	1000000.0	1000000.0
MP03001	MAL3P2.11	386	CAB38998	99.0010	LIMVLSFLFL	10	1000000.0	38.4	1000000.0	1000000.0
MP03001	MAL3P2.11	318	CAB38998	99.0065	YLNKIQNSL	9	13496.2	78.4	1000000.0	1000000.0
MP03001	MAL3P2.11	387	CAB38998	99.0066	IMVLSFLFL	9	8739.3	36.0	1000000.0	2608.6
1369.t00001	Chromosome 11	60		99.0011	VQMMIMIKFM	10	1000000.0	96.6	1000000.0	1000000.0
1369.t00001	Chromosome 11	62		99.0012	MMIMIKFMGV	10	1000000.0	47.1	1000000.0	1000000.0
1369.t00001	Chromosome 11	9		99.0067	KIYKIIIWI	9	56576.0	72.2	1000000.0	1000000.0
1369.t00001	Chromosome 11	23		99.0068	YMIKKLLKI	9	4324.7	52.7	1000000.0	788.9
1369.t00001	Chromosome 11	42		99.0069	LMTLYQIQV	9	32880.1	41.7	1000000.0	1000000.0
1369.t00001	Chromosome 11	68		99.0070	FMGVIYIMI	9	10136.0	91.9	1000000.0	58.6
1369.t00001	Chromosome 11	280		99.0071	NILIVLYYL	9	117610.0	42.8	1000000.0	1000000.0
1369.t00001	Chromosome 11	312		99.0072	FMNRFYITT	9	14073.8	47.8	1000000.0	1000000.0
699.t00001	Chromosome 11	488		99.0013	YLYISFLLLI	10	311433.0	34.2	1000000.0	1000000.0
699.t00001	Chromosome 11	1025		99.0014	YIYIFIYLFI	10	1000000.0	19.8	1000000.0	1000000.0
699.t00001	Chromosome 11	408		99.0073	LLDDYHFET	9	5923.7	39.5	1000000.0	1000000.0
699.t00001	Chromosome 11	488		99.0074	YLYISFLLL	9	2547.9	11.2	1000000.0	1000000.0
699.t00001	Chromosome 11	572		99.0075	FLTLTVYPI	9	22535.9	28.3	1000000.0	1000000.0
699.t00001	Chromosome 11	651		99.0076	FIIEILELL	9	15575.2	47.0	1000000.0	1000000.0
699.t00001	Chromosome 11	782		99.0077	LLYNHITSI	9	62668.0	50.4	1000000.0	1000000.0
699.t00001	Chromosome 11	882		99.0078	YMNFLKFIV	9	14215.9	50.3	1000000.0	1000000.0
699.t00001	Chromosome 11	1033		99.0079	FIYIWLHLI	9	6243.9	15.6	1000000.0	1000000.0
699.t00001	Chromosome 11	1039		99.0080	HLIIIFIFV	9	6908.2	11.5	1000000.0	1000000.0
M13Hg2.q1t3		576		99.0015	FLMWSSQIII	10	96042.7	91.8	1000000.0	1000000.0
M13Hg2.q1t3		96		99.0081	ILLSRFIFI	9	11278.3	22.9	1000000.0	1000000.0

Table 4:
Pf-derived A2 supertype peptides with PIC <100nM

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101	A*2402
M13Hg2.q1t3		508		99.0082	YLNFQDNYL	9	34942.8	80.6	1000000.0	1000000.0
M13Hg2.q1t3		551		99.0083	NIPYFNFFV	9	86593.7	41.8	1000000.0	1000000.0
M13Hg2.q1t3		558		99.0084	FVNYFEAVV	9	15474.4	100.0	1000000.0	1000000.0
M13Hg2.q1t3		569		99.0085	NIHCYTYFL	9	27934.2	25.6	1000000.0	1000000.0
M13Hg2.q1t3		576		99.0086	FLMWSSQII	9	5275.5	31.9	1000000.0	1000000.0
M13Hg2.q1t3		577		99.0087	LMWSSQIII	9	15320.6	46.4	1000000.0	614.0
M13Hg2.q1t3		723		99.0088	ILNKISSFV	9	17591.1	89.9	1000000.0	1000000.0
Mal_5L10c4.q1t6		334		99.0089	FVFFIIKNV	9	13366.7	53.5	1000000.0	1000000.0
Mal_5L10c4.q1t6		366		99.0090	IQICKLYHV	9	8534.4	35.2	1000000.0	1000000.0
Mal_5L10c4.q1t6		534		99.0091	YISSVNYFL	9	25585.7	24.2	1000000.0	1000000.0
Mal_5L10c4.q1t6		1205		99.0092	YLFQLVQSL	9	4424.1	26.3	1000000.0	1000000.0
Mal_5L10c4.q1t6		1240		99.0093	SIYFYWFLL	9	13813.9	27.2	1000000.0	1000000.0
Mal_5L10c4.q1t6		1260		99.0094	YLHIHKLFI	9	46175.4	47.6	1000000.0	1000000.0
Mal_5L10c4.q1t6		1596		99.0095	ILDDSINFV	9	8148.9	41.5	1000000.0	1000000.0
Mal_5L10c4.q1t6		1629		99.0096	FLPEQSYVL	9	36294.8	55.0	1000000.0	1000000.0
Mal_5L10c4.q1t6		1890		99.0097	HLVIQIIYV	9	52344.4	36.6	1000000.0	1000000.0
Mal_5L10c4.q1t6		2106		99.0098	FLSVINASV	9	15607.8	17.1	1000000.0	1000000.0
571.t00003	Chromosome11	105		99.0016	ILYPSLMPYV	10	1000000.0	81.0	1000000.0	1000000.0
571.t00003	Chromosome11	2443		99.0017	YLFGKVKFYI	10	821413.1	47.5	1000000.0	1000000.0
571.t00003	Chromosome11	68		99.0099	KLINTNFYI	9	109718.5	49.2	1000000.0	1000000.0
571.t00003	Chromosome11	92		99.0100	KTFIYSNFL	9	34260.6	95.5	1000000.0	1000000.0
571.t00003	Chromosome11	109		99.0101	SLMPYVECI	9	3307.6	80.4	1000000.0	1000000.0
571.t00003	Chromosome11	163		99.0102	YTNYYQSFI	9	14053.9	63.6	1000000.0	1000000.0
571.t00003	Chromosome11	1224		99.0103	FQWEKSNKI	9	17731.1	88.1	1000000.0	1000000.0
571.t00003	Chromosome11	1330		99.0104	FLIKLNNEI	9	32980.5	73.6	1000000.0	1000000.0
571.t00003	Chromosome11	1478		99.0105	YMYTNYLNM	9	5105.1	65.8	1000000.0	4545.4
571.t00003	Chromosome11	2286		99.0106	FQGEYVSNL	9	28240.4	61.4	1000000.0	1000000.0
MP03072	PFC0450w	7	CAA15614	99.0018	ILILIDAASV	10	1000000.0	88.5	1000000.0	1000000.0

Table 4:
Pf-derived A2 supertype peptides with PIC <100nM

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101	A*2402
MP03072	PFC0450w	19	CAA15614	99.0019	LLITFLMINL	10	1000000.0	82.3	1000000.0	1000000.0
MP03072	PFC0450w	46	CAA15614	99.0020	ALVVAIILYV	10	599232.7	38.0	1000000.0	1000000.0
MP03072	PFC0450w	50	CAA15614	99.0021	AIILYVIFLV	10	1000000.0	58.1	1000000.0	1000000.0
MP03072	PFC0450w	52	CAA15614	99.0022	ILYVIFLVLL	10	1000000.0	33.8	1000000.0	1000000.0
MP03072	PFC0450w	54	CAA15614	99.0023	YVIFLVLLFI	10	656413.8	20.3	1000000.0	1000000.0
MP03072	PFC0450w	57	CAA15614	99.0024	FLVLLFIYKA	10	139.6	80.7	498.9	1000000.0
MP03072	PFC0450w	18	CAA15614	99.0107	FLLITFLMI	9	5377.9	28.0	1000000.0	1000000.0
MP03072	PFC0450w	47	CAA15614	99.0108	LVVAIILYV	9	17753.4	20.8	1000000.0	1000000.0
MP03072	PFC0450w	50	CAA15614	99.0109	AIILYVIFL	9	35558.1	23.3	1000000.0	1000000.0
MP03072	PFC0450w	51	CAA15614	99.0110	IILYVIFLV	9	29081.2	23.4	1000000.0	1000000.0
MP03072	PFC0450w	52	CAA15614	99.0111	ILYVIFLVL	9	4626.7	49.4	1000000.0	1000000.0
MP03072	PFC0450w	55	CAA15614	99.0112	VIFLVLLFI	9	17063.1	28.6	1000000.0	1000000.0
45.t00001	Chromosome14	22		99.0113	YQDPQNYEL	9	17446.7	62.2	1000000.0	1000000.0
45.t00001	Chromosome14	134		99.0114	KTWKPTIFL	9	18939.7	82.8	1000000.0	1000000.0
45.t00001	Chromosome14	142		99.0115	LLNESNIFL	9	13381.3	66.8	1000000.0	1000000.0
45.t00001	Chromosome14	220		99.0116	FIHFFTWGT	9	54429.1	69.2	1000000.0	1000000.0
MP03137	PFC0700c	180	CAB11150	99.0117	VLFLQMMNV	9	71815.8	72.3	1000000.0	1000000.0
MP03137	PFC0700c	251	CAB11150	99.0118	NQMIFVSSI	9	39082.0	99.1	1000000.0	1000000.0
MP03137	PFC0700c	253	CAB11150	99.0119	MIFVSSIFI	9	17820.1	95.9	1000000.0	1000000.0
MP03137	PFC0700c	258	CAB11150	99.0120	SIFISFYLI	9	13357.1	72.3	1000000.0	1000000.0
MP03137	PFC0700c	293	CAB11150	99.0121	RLFEESLGI	9	22704.6	90.4	1000000.0	1000000.0
12.t00018	Chromosome14	870		99.0025	YLCLYNGLLL	10	294216.7	79.1	1000000.0	1000000.0
12.t00018	Chromosome14	1018		99.0026	YLLFFREKFL	10	1000000.0	57.8	1000000.0	1000000.0

Table 4:
Pf-derived A2 supertype peptides with PIC <100nM

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101	A*2402
12.t00018	Chromosome14	597		99.0122	KLIEYFLNM	9	8556.1	30.0	1000000.0	1000000.0
12.t00018	Chromosome14	615		99.0123	YVSMYIPFI	9	7367.7	57.9	1000000.0	1000000.0
12.t00018	Chromosome14	870		99.0124	YLCLYNGLL	9	12899.1	68.8	1000000.0	1000000.0
12.t00018	Chromosome14	893		99.0125	NIISSIFYI	9	94922.9	77.9	1000000.0	1000000.0
12.t00018	Chromosome14	907		99.0126	YLYDNYSHL	9	11094.9	55.2	1000000.0	1000000.0
12.t00018	Chromosome14	953		99.0127	FLNVYENFL	9	23398.0	34.3	1000000.0	1000000.0
12.t00018	Chromosome14	1037		99.0128	LIFGYNSLI	9	26493.2	50.1	1000000.0	1000000.0
12.t00018	Chromosome14	1047		99.0129	FLFYGCREV	9	24096.2	30.4	1000000.0	1000000.0
mal_BU121g9.q1c1		90		99.0130	YIYIYIYFL	9	32096.6	3.8	1000000.0	1000000.0
mal_BU121g9.q1c1		92		99.0131	YIYIYFLQI	9	15022.6	13.6	1000000.0	1000000.0
mal_9A57b11.q1t2		138		99.0132	KQYTDIPSL	9	184531.0	81.9	1000000.0	1000000.0
mal_9A57b11.q1t2		158		99.0133	KVFCYEYFI	9	10650.1	18.0	1000000.0	1000000.0
mal_9A57b11.q1t2		165		99.0134	FIFDIFKYA	9	21.1	20.2	44.0	1000000.0
mal_BL50e8.p1ca_5		6		99.0027	ALLSFLVVLV	10	1000000.0	42.5	1000000.0	1000000.0
mal_BL50e8.p1ca_5		65		99.0028	RQINFMETFV	10	1000000.0	54.6	1000000.0	1000000.0
mal_BL50e8.p1ca_5		4		99.0135	FVALLSFLV	9	3130.0	26.0	1000000.0	1000000.0
mal_BL50e8.p1ca_5		7		99.0136	LLSFLVVLV	9	11579.5	36.2	1000000.0	1000000.0
mal_BL50e8.p1ca_5		192		99.0137	FIYNWVLQT	9	30528.1	55.9	1000000.0	1000000.0
mal_BL50e8.p1ca_5		349		99.0138	ILIRALLSL	9	8963.2	44.4	1000000.0	1000000.0
mal_BL50e8.p1ca_5		353		99.0139	ALLSLDFSL	9	22110.4	36.6	1000000.0	1000000.0
mal_BL50e8.p1ca_5		562		99.0140	NLFGGGFYI	9	22065.3	23.4	1000000.0	1000000.0
mal_BL50e8.p1ca_5		779		99.0141	LMLKADYFI	9	22456.0	21.9	1000000.0	444.0
mal_BL50e8.p1ca_5		973		99.0142	NIYTHSVYV	9	245555.5	53.7	1000000.0	1000000.0
M13S8h6.p1t_3		7		99.0143	FVLACVLLI	9	10293.7	14.2	1000000.0	1000000.0
M13S8h6.p1t_3		23		99.0144	ATSTFFFFL	9	3703.8	20.0	1000000.0	1000000.0
M13S8h6.p1t_3		34		99.0145	FLLICGFCI	9	23058.3	21.3	1000000.0	1000000.0
M13S8h6.p1t_3		55		99.0146	VLITYSFTV	9	35516.3	7.8	1000000.0	1000000.0
M13S8h6.p1t_3		61		99.0147	FTVSYIFFM	9	18627.5	9.0	1000000.0	1000000.0

Table 4:
Pf-derived A2 supertype peptides with PIC <100nM

Docket No.: EPI-103X

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Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101	A*2402
M13S8h6.p1t_3		77		99.0148	LLVCISILL	9	4378.4	24.2	1000000.0	1000000.0
M13S8h6.p1t_3		1447		99.0149	FIITYIWII	9	50315.1	20.9	1000000.0	1000000.0
M13S8h6.p1t_3		1469		99.0150	KMMWTIFIL	9	13621.2	14.7	1000000.0	35.6
M13S8h6.p1t_3		1538		99.0151	FVFFYIFLI	9	5681.7	3.2	1000000.0	1000000.0
M13S8h6.p1t_3		1582		99.0152	YLDRIQFLV	9	3212.4	6.0	1000000.0	1000000.0
585.t00002	Chromosome11	651		99.0029	VLSPFSLIFV	10	236320.1	33.8	1000000.0	1000000.0
585.t00002	Chromosome11	1380		99.0030	TLVNILILFL	10	1000000.0	25.5	1000000.0	1000000.0
585.t00002	Chromosome11	1406		99.0031	FVFFRFLFFV	10	132657.2	16.7	1000000.0	1000000.0
585.t00002	Chromosome11	6		99.0153	FILFYFYVM	9	18702.2	16.8	1000000.0	1000000.0
585.t00002	Chromosome11	17		99.0154	YTFCFLPVL	9	3159.4	24.6	1000000.0	1000000.0
585.t00002	Chromosome11	643		99.0155	WLFFFDLVV	9	13858.2	39.1	1000000.0	1000000.0
585.t00002	Chromosome11	661		99.0156	HLFFCIFFI	9	13336.6	6.4	1000000.0	1000000.0
585.t00002	Chromosome11	1386		99.0157	ILFLICYSI	9	18185.7	17.8	1000000.0	1000000.0
585.t00002	Chromosome11	1399		99.0158	YMFSYIPFV	9	20964.1	1.1	1000000.0	1000000.0
585.t00002	Chromosome11	1507		99.0159	YILFILFFI	9	12765.9	4.2	1000000.0	1000000.0
1223.t00015	mal_9A21f9.q1t_4	1387		99.0032	LIHDDVLLFL	10	1000000.0	32.2	1000000.0	1000000.0
1223.t00015	mal_9A21f9.q1t_4	270		99.0160	FVSFYKFEV	9	10792.4	28.2	1000000.0	1000000.0
1223.t00015	mal_9A21f9.q1t_4	811		99.0161	MLWCSMESV	9	5755.3	27.5	1000000.0	1000000.0
1223.t00015	mal_9A21f9.q1t_4	924		99.0162	KLFDAINYL	9	35603.1	20.5	1000000.0	1000000.0
1223.t00015	mal_9A21f9.q1t_4	1648		99.0163	FVMDITDSI	9	4215.8	44.1	1000000.0	1000000.0
1223.t00015	mal_9A21f9.q1t_4	1853		99.0164	MLYSIVWGL	9	18338.7	24.8	1000000.0	1000000.0
1223.t00015	mal_9A21f9.q1t_4	2301		99.0165	NIYFSYFYV	9	68948.8	41.1	1000000.0	1000000.0
1223.t00015	mal_9A21f9.q1t_4	2548		99.0166	FILEHVNSI	9	80628.8	42.2	1000000.0	1000000.0
1223.t00015	mal_9A21f9.q1t_4	3057		99.0167	SLLKAQLFV	9	12372.4	15.7	1000000.0	1000000.0
1223.t00015	mal_9A21f9.q1t_4	4419		99.0168	SLDEVVLYT	9	8137.8	46.3	1000000.0	1000000.0
599.t00001	Chromosome11	1069		99.0033	HLMHIINVFI	10	1000000.0	56.9	1000000.0	1000000.0
599.t00001	Chromosome11	1341		99.0034	FLSDYTTCSV	10	93945.4	72.2	1000000.0	1000000.0
599.t00001	Chromosome11	1458		99.0035	FLRNYVVIFI	10	615882.5	83.6	1000000.0	1000000.0

Table 4:
Pf-derived A2 supertype peptides with PIC <100nM

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599.t00001	Chromosome11	9		99.0169	YLTINFFIL	9	4373.8	64.1	1000000.0	1000000.0
599.t00001	Chromosome11	883		99.0170	NMNDIENFV	9	32886.3	78.0	1000000.0	1000000.0
599.t00001	Chromosome11	1013		99.0171	FIHDILLDL	9	11903.4	46.8	1000000.0	1000000.0
599.t00001	Chromosome11	1034		99.0172	NQYAYDLKI	9	38604.8	81.2	1000000.0	1000000.0
599.t00001	Chromosome11	1718		99.0173	GLGGLLFII	9	5216.8	74.2	1000000.0	1000000.0
599.t00001	Chromosome11	1770		99.0174	YIMNNTIFT	9	4444.5	75.2	1000000.0	1000000.0
599.t00001	Chromosome11	1914		99.0175	HLFNFSNFV	9	16629.7	25.5	1000000.0	1000000.0
MP01072	M1045c5.p1c.C_6	1138		99.0036	YLIRNILMSI	10	819635.3	75.5	1000000.0	1000000.0
MP01072	M1045c5.p1c.C_6	66		99.0176	YLYKSIFKA	9	6.2	29.5	1755.3	1000000.0
MP01072	M1045c5.p1c.C_6	82		99.0177	YLDFYEFCV	9	5138.7	6.7	1000000.0	1000000.0
MP01072	M1045c5.p1c.C_6	1161		99.0178	KIFFLFFSI	9	19713.1	22.7	1000000.0	1000000.0
MP01072	M1045c5.p1c.C_6	1281		99.0179	KLNEINILL	9	15599.8	69.4	1000000.0	1000000.0
PIR2	T28161	577		99.0037	FLMFWVAHML	10	60152.9	33.4	1000000.0	1000000.0
PIR2	T28161	142		99.0180	LLAEVCYAA	9	9.8	35.1	4774.0	1000000.0
PIR2	T28161	369		99.0181	CLYVCDPYV	9	78244.5	58.0	1000000.0	1000000.0
PIR2	T28161	577		99.0182	FLMFWVAHM	9	3061.0	5.7	1000000.0	1000000.0
PIR2	T28161	642		99.0183	FQGWGHYFV	9	53546.0	13.8	1000000.0	1000000.0
PIR2	T28161	888		99.0184	FLGDVLFAA	9	6.7	8.3	2549.7	1000000.0
PIR2	T28161	892		99.0185	VLFAANYEA	9	25.8	20.9	100.0	1000000.0
PIR2	T28161	1098		99.0186	YLQAQTTAA	9	26.9	64.0	17290.2	1000000.0
PIR2	T28161	1461		99.0187	FLRQMFYTL	9	8779.8	60.8	1000000.0	1000000.0
PIR2	T28161	2149		99.0188	FAAFTYFYL	9	11639.0	45.5	1000000.0	1000000.0
55.t00004	Chromosome14	1358		99.0038	FMDSQNGMYI	10	26503.4	87.2	1000000.0	4109.6
55.t00004	Chromosome14	1542		99.0039	SLINYNKYFV	10	1000000.0	43.5	1000000.0	1000000.0
55.t00004	Chromosome14	84		99.0189	FVVAQLYEL	9	27995.5	19.7	1000000.0	1000000.0
55.t00004	Chromosome14	480		99.0190	KTFFFFSNV	9	10931.8	72.4	1000000.0	1000000.0
55.t00004	Chromosome14	1098		99.0191	IINSDDYFV	9	58940.8	86.9	1000000.0	1000000.0
55.t00004	Chromosome14	1364		99.0192	GMYILPQYV	9	18255.9	74.7	1000000.0	1000000.0

Table 4:
Pf-derived A2 supertype peptides with PIC <100nM

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101	A*2402
674.t00001	Chromosome11	89		99.0040	ELVEFIFLLL	10	1000000.0	97.4	1000000.0	1000000.0
674.t00001	Chromosome11	281		99.0041	FLYKDVLMDI	10	358012.1	50.4	1000000.0	1000000.0
674.t00001	Chromosome11	89		99.0193	ELVEFIFLL	9	21772.0	47.1	1000000.0	1000000.0
674.t00001	Chromosome11	1102		99.0194	YLNKANPNI	9	12319.8	91.3	1000000.0	1000000.0
674.t00001	Chromosome11	1353		99.0195	FLQYRIPHM	9	33178.8	81.0	1000000.0	1000000.0
674.t00001	Chromosome11	1430		99.0196	YIVDIFCKI	9	11720.4	48.5	1000000.0	1000000.0

Table 5:
Pf-derived A3,11 supertype peptides scoring positive on PIC algorithm

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101 PIC	A*2402
331.t00003	Chromosome10	354		99.0197	KFEPFIIHVK	10	1000000.0	1000000.0	26.5	1000000.0
331.t00003	Chromosome10	5		99.0294	KTMDTFYKK	9	2654.1	1000000.0	0.4	1000000.0
331.t00003	Chromosome10	208		99.0295	SFFDVSKKK	9	130857.6	1000000.0	16.4	1000000.0
331.t00003	Chromosome10	435		99.0296	LSQLVHFYK	9	29656.2	1000000.0	0.6	1000000.0
331.t00003	Chromosome10	779		99.0297	SVFVRRYIK	9	18991.0	1000000.0	0.7	1000000.0
331.t00003	Chromosome10	988		99.0298	FTFQNMYVR	9	5834.2	1000000.0	22.0	1000000.0
331.t00003	Chromosome10	1324		99.0299	SQNSNTFLK	9	10099.5	1000000.0	0.4	1000000.0
331.t00003	Chromosome10	1337		99.0300	ILFHKFLNK	9	3064.6	1000000.0	2.4	1000000.0
331.t00003	Chromosome10	1521		99.0301	NLFDENFCR	9	30418.9	1000000.0	165.9	1000000.0
331.t00003	Chromosome10	1551		99.0302	ALYEKVHGK	9	9346.6	1000000.0	4.4	1000000.0
18.000811	Chr12Contig18	17		99.0198	FLLYILFLVK	10	1000000.0	1000000.0	82.1	1000000.0
18.000811	Chr12Contig18	43		99.0199	LVFSNVLCFR	10	365585.5	1000000.0	14.5	1000000.0
18.000811	Chr12Contig18	80		99.0200	AFLESQSMNK	10	1000000.0	1000000.0	65.8	1000000.0
18.000811	Chr12Contig18	112		99.0201	TFLESSFDIK	10	1000000.0	1000000.0	323.9	1000000.0
18.000811	Chr12Contig18	116		99.0202	SSFDIKSEVK	10	1000000.0	1000000.0	34.1	1000000.0
18.000811	Chr12Contig18	18		99.0303	LLYILFLVK	9	5498.6	1000000.0	10.1	1000000.0
18.000811	Chr12Contig18	129		99.0304	KSMLKELIK	9	5942.8	1000000.0	12.7	1000000.0
18.000811	Chr12Contig18	166		99.0305	PVLTSLFNK	9	10202.9	1000000.0	10.1	1000000.0
MY924Fe3.pltl		1262		99.0203	TFICYYVMDK	10	1000000.0	1000000.0	23.0	1000000.0
MY924Fe3.pltl		155		99.0306	NVFNIFFEK	9	10371.8	1000000.0	0.2	1000000.0
MY924Fe3.pltl		220		99.0307	SSFLYAFNK	9	12434.3	1000000.0	0.1	1000000.0
MY924Fe3.pltl		1030		99.0308	MFHIIMYTK	9	208352.1	1000000.0	18.2	1000000.0
MY924Fe3.pltl		1181		99.0309	SLDDIYKYK	9	22644.9	1000000.0	2.9	1000000.0
MY924Fe3.pltl		1613		99.0310	KVVVKNLYK	9	34654.1	1000000.0	0.9	1000000.0
MY924Fe3.pltl		1853		99.0311	SLFRLGFVK	9	10283.0	1000000.0	0.2	1000000.0
MY924Fe3.pltl		2012		99.0312	SLFFNSLYY	9	4.6	1000000.0	2.6	1000000.0
MY924Fe3.pltl		2238		99.0313	ITFEKNYYR	9	21591.6	1000000.0	1.5	1000000.0

Table 5:
Pf-derived A3,11 supertype peptides scoring positive on PIC algorithm

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101 PIC	A*2402
MY924Fe3.pltl		2285		99.0314	SQYEENKSK	9	139775.3	1000000.0	39.1	1000000.0
MP03001	MAL3P2.11	57	CAB38998	99.0204	KQENWYSLKK	10	1000000.0	1000000.0	50.6	1000000.0
MP03001	MAL3P2.11	335	CAB38998	99.0205	VTCGNGIQVR	10	1000000.0	1000000.0	170.6	1000000.0
MP03001	MAL3P2.11	17	CAB38998	99.0315	ALFQEYQCY	9	3.4	1000000.0	72.7	1000000.0
MP03001	MAL3P2.11	57	CAB38998	99.0316	KQENWYSLK	9	44996.2	1000000.0	173.7	1000000.0
1369.t00001	Chromosome 11	44		99.0206	TLYQIQVMKR	10	1000000.0	1000000.0	52.0	1000000.0
1369.t00001	Chromosome 11	58		99.0207	KQVQMMIMIK	10	1000000.0	1000000.0	8.7	1000000.0
1369.t00001	Chromosome 11	70		99.0208	GVIYIMIISK	10	1000000.0	1000000.0	10.6	1000000.0
1369.t00001	Chromosome 11	158		99.0209	ELFDKDTFFK	10	1000000.0	1000000.0	14.2	1000000.0
1369.t00001	Chromosome 11	18		99.0317	KTMNNYMIK	9	16730.1	1000000.0	1.1	1000000.0
1369.t00001	Chromosome 11	159		99.0318	LFDKDTFFK	9	32977.1	1000000.0	126.3	1000000.0
1369.t00001	Chromosome 11	287		99.0319	YLFNQHIKK	9	21347.4	1000000.0	8.2	1000000.0
1369.t00001	Chromosome 11	307		99.0320	MQSSFFMNR	9	12685.3	1000000.0	25.4	1000000.0
1369.t00001	Chromosome 11	315		99.0321	RFYITTRYK	9	258367.4	1000000.0	21.4	1000000.0
1369.t00001	Chromosome 11	319		99.0322	TTRYKYLNK	9	10429.2	1000000.0	4.5	1000000.0
699.t00001	Chromosome 11	464		99.0210	KVCELLGYYK	10	1000000.0	1000000.0	1.1	1000000.0
699.t00001	Chromosome 11	492		99.0211	SFLLLIVFSK	10	1000000.0	1000000.0	21.9	1000000.0
699.t00001	Chromosome 11	623		99.0212	KLLYKMNYLK	10	1000000.0	1000000.0	15.0	1000000.0
699.t00001	Chromosome 11	764		99.0213	TLEYNPSFFY	10	91.9	1000000.0	219.0	1000000.0
699.t00001	Chromosome 11	782		99.0214	LLYNHITSIK	10	1000000.0	1000000.0	12.1	1000000.0
699.t00001	Chromosome 11	878		99.0215	LFYLYMNFLK	10	1000000.0	1000000.0	8.2	1000000.0
699.t00001	Chromosome 11	386		99.0323	KQNIPIYIY	9	57.8	1000000.0	175.4	1000000.0
699.t00001	Chromosome 11	507		99.0324	KTNIFFKKK	9	23058.6	1000000.0	1.5	1000000.0
699.t00001	Chromosome 11	734		99.0325	IVNDLGIFY	9	2.4	1000000.0	16.6	1000000.0
699.t00001	Chromosome 11	769		99.0326	PSFFYLSFK	9	22074.6	1000000.0	20.1	1000000.0
mal_4T2c4.pltl		15		99.0216	ILLIRPMLVK	10	1000000.0	1000000.0	95.1	1000000.0
mal_4T2c4.pltl		29		99.0217	LVKLRPMLVK	10	1000000.0	1000000.0	22.3	1000000.0

Table 5:
Pf-derived A3,11 supertype peptides scoring positive on PIC algorithm

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101 PIC	A*2402
mal_4T2c4.pltl		36		99.0218	LVKLGPILVK	10	1000000.0	1000000.0	15.0	1000000.0
mal_4T2c4.pltl		16		99.0327	LLIRPMLVK	9	29115.0	1000000.0	16.1	1000000.0
M13Hg2.qlt3		97		99.0219	LLSRFIFIYK	10	1000000.0	1000000.0	12.9	1000000.0
M13Hg2.qlt3		267		99.0220	KTSDAKLVDK	10	543207.5	1000000.0	21.8	1000000.0
M13Hg2.qlt3		277		99.0221	ETSTISTFIK	10	714638.7	1000000.0	21.8	1000000.0
M13Hg2.qlt3		406		99.0222	IFFSYNPFHK	10	1000000.0	1000000.0	18.5	1000000.0
M13Hg2.qlt3		528		99.0223	YFFNCIQMAK	10	1000000.0	1000000.0	48.6	1000000.0
M13Hg2.qlt3		9		99.0328	SLYNKIEYR	9	32837.9	1000000.0	36.8	1000000.0
M13Hg2.qlt3		48		99.0329	SASESNFYK	9	17208.3	1000000.0	0.2	1000000.0
M13Hg2.qlt3		216		99.0330	ISYIFPLFK	9	12671.6	1000000.0	2.2	1000000.0
M13Hg2.qlt3		420		99.0331	SQNYENINK	9	36248.0	1000000.0	3.6	1000000.0
M13Hg2.qlt3		661		99.0332	SLMDASKNK	9	5327.4	1000000.0	3.2	1000000.0
Mal_5L10c4.qlt6		21		99.0333	KLGFFVCYK	9	42997.2	1000000.0	3.5	1000000.0
Mal_5L10c4.qlt6		36		99.0334	SFKNKILQK	9	139254.7	1000000.0	14.9	1000000.0
Mal_5L10c4.qlt6		56		99.0335	KFMYLRKKK	9	74875.0	1000000.0	33.4	1000000.0
Mal_5L10c4.qlt6		381		99.0336	KQIIFEALK	9	120283.5	1000000.0	38.9	1000000.0
Mal_5L10c4.qlt6		519		99.0337	ETFYKELYK	9	14646.9	1000000.0	1.2	1000000.0
Mal_5L10c4.qlt6		537		99.0338	SVNYFLLER	9	4574.8	1000000.0	0.4	1000000.0
Mal_5L10c4.qlt6		724		99.0339	ILNFLNFNK	9	12039.7	1000000.0	2.7	1000000.0
Mal_5L10c4.qlt6		897		99.0340	NTCSKEIYK	9	26259.6	1000000.0	4.6	1000000.0
Mal_5L10c4.qlt6		1316		99.0341	KLRNFLFYY	9	34.8	1000000.0	27.7	1000000.0
Mal_5L10c4.qlt6		1722		99.0342	CSNNNIFYK	9	16887.2	1000000.0	2.7	1000000.0
571.t00003	Chromosome11	1059		99.0224	MQYNHDNIYK	10	1000000.0	1000000.0	6.8	1000000.0
571.t00003	Chromosome11	2438		99.0225	SFSMLYLFGK	10	1000000.0	1000000.0	20.1	1000000.0
571.t00003	Chromosome11	675		99.0343	ALNPKYQNH	9	4302.1	1000000.0	149.6	1000000.0
571.t00003	Chromosome11	749		99.0344	TLNSFQHNK	9	9140.5	1000000.0	4.0	1000000.0
571.t00003	Chromosome11	1220		99.0345	KINEFQWEK	9	55899.8	1000000.0	0.3	1000000.0

Table 5:
Pf-derived A3,11 supertype peptides scoring positive on PIC algorithm

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101 PIC	A*2402
571.t00003	Chromosome11	1368		99.0346	RSDYFHNTK	9	15625.8	1000000.0	5.2	1000000.0
571.t00003	Chromosome11	1429		99.0347	STNSQQLIK	9	14992.1	1000000.0	1.1	1000000.0
571.t00003	Chromosome11	1552		99.0348	KFMTPTTLK	9	54389.6	1000000.0	8.1	1000000.0
571.t00003	Chromosome11	1684		99.0349	TTNSTPHFK	9	5905.8	1000000.0	3.8	1000000.0
571.t00003	Chromosome11	2509		99.0350	KLMETRFSK	9	8313.3	1000000.0	2.8	1000000.0
MP03072	PFC0450w	36	CAA15614	99.0226	SQAHRENGKK	10	1000000.0	1000000.0	109.2	1000000.0
MP03072	PFC0450w	45	CAA15614	99.0227	KALVVAIILY	10	220.1	1000000.0	237.1	1000000.0
MP03072	PFC0450w	55	CAA15614	99.0228	VIFLVLLFIY	10	137.2	1000000.0	61.8	1000000.0
MP03072	PFC0450w	56	CAA15614	99.0229	IFLVLLFIYK	10	1000000.0	1000000.0	44.3	1000000.0
MP03072	PFC0450w	58	CAA15614	99.0230	LVLLFIYKAY	10	371.7	1000000.0	207.5	1000000.0
MP03072	PFC0450w	59	CAA15614	99.0231	VLLFIYKAYK	10	1000000.0	1000000.0	31.2	1000000.0
MP03072	PFC0450w	61	CAA15614	99.0232	LFIYKAYKNK	10	1000000.0	1000000.0	434.4	1000000.0
MP03072	PFC0450w	72	CAA15614	99.0233	KLYTNFFMKK	10	1000000.0	1000000.0	5.8	1000000.0
MP03072	PFC0450w	92	CAA15614	99.0234	STYLSASDEY	10	57.2	1000000.0	85.1	1000000.0
MP03072	PFC0450w	36	CAA15614	99.0351	SQAHRENGK	9	65339.9	1000000.0	230.0	1000000.0
MP03072	PFC0450w	46	CAA15614	99.0352	ALVVAIILY	9	6.0	1000000.0	95.4	1000000.0
MP03072	PFC0450w	57	CAA15614	99.0353	FLVLLFIYK	9	14940.5	1000000.0	5.0	1000000.0
MP03072	PFC0450w	58	CAA15614	99.0354	LVLLFIYKA	9	13.1	102.2	132.5	1000000.0
MP03072	PFC0450w	60	CAA15614	99.0355	LLFIYKAYK	9	59055.3	1000000.0	9.6	1000000.0
MP03072	PFC0450w	62	CAA15614	99.0356	FIYKAYKNK	9	35013.8	1000000.0	22.0	1000000.0
MP03072	PFC0450w	72	CAA15614	99.0357	KLYTNFFMK	9	7491.5	1000000.0	2.3	1000000.0
MP03072	PFC0450w	74	CAA15614	99.0358	YTNFFMKKR	9	18478.3	1000000.0	48.4	1000000.0
45.t00001	Chromosome14	50		99.0235	ALERLLSLKK	10	1000000.0	1000000.0	149.5	1000000.0
45.t00001	Chromosome14	109		99.0236	KILIKIPVTK	10	1000000.0	1000000.0	30.2	1000000.0
45.t00001	Chromosome14	128		99.0237	RLPLLPKTWK	10	1000000.0	1000000.0	19.6	1000000.0
45.t00001	Chromosome14	147		99.0238	NIFLRFIPDK	10	1000000.0	1000000.0	24.9	1000000.0
45.t00001	Chromosome14	161		99.0239	SQVSNSDSYK	10	1000000.0	1000000.0	36.0	1000000.0
45.t00001	Chromosome14	197		99.0240	QQNQESKIMK	10	928526.9	1000000.0	431.5	1000000.0

Table 5:
Pf-derived A3,11 supertype peptides scoring positive on PIC algorithm

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101 PIC	A*2402
45.t00001	Chromosome14	249		99.0241	IIALLIIPPK	10	1000000.0	1000000.0	19.3	1000000.0
45.t00001	Chromosome14	374		99.0242	SQDLACIFDA	10	226.7	389.1	400.3	1000000.0
45.t00001	Chromosome14	34		99.0359	AVIFTPIYY	9	7.6	1000000.0	4.7	1000000.0
45.t00001	Chromosome14	50		99.0360	ALERLLSLK	9	6245.7	1000000.0	55.5	1000000.0
45.t00001	Chromosome14	85		99.0361	SISGKYDIK	9	29562.3	1000000.0	25.1	1000000.0
45.t00001	Chromosome14	101		99.0362	ILCIEGEQK	9	51943.1	1000000.0	162.5	1000000.0
45.t00001	Chromosome14	126		99.0363	EQRLPLLPK	9	66848.0	1000000.0	244.3	1000000.0
45.t00001	Chromosome14	148		99.0364	IFLRFIPDK	9	170326.8	1000000.0	112.0	1000000.0
45.t00001	Chromosome14	250		99.0365	IALLIIPPK	9	47443.5	1000000.0	25.2	1000000.0
45.t00001	Chromosome14	270		99.0366	PVVCSMEYK	9	20870.3	1000000.0	23.1	1000000.0
45.t00001	Chromosome14	271		99.0367	VVCSMEYKK	9	24792.5	1000000.0	8.3	1000000.0
45.t00001	Chromosome14	308		99.0368	FSYDLRLNK	9	5228.9	1000000.0	13.4	1000000.0
45.t00001	Chromosome14	323		99.0369	HLNIPIGFK	9	25082.0	1000000.0	98.3	1000000.0
MP03137	PFC0700c	14	CAB11150	99.0243	SSPLFNNFYK	10	1000000.0	1000000.0	0.5	1000000.0
MP03137	PFC0700c	151	CAB11150	99.0244	FLYLLNKKNK	10	1000000.0	1000000.0	139.2	1000000.0
MP03137	PFC0700c	183	CAB11150	99.0245	LQMMNVNLQK	10	1000000.0	1000000.0	83.6	1000000.0
MP03137	PFC0700c	195	CAB11150	99.0246	LTNHLINTPK	10	427675.0	1000000.0	20.8	1000000.0
MP03137	PFC0700c	259	CAB11150	99.0247	IFISFYLINK	10	1000000.0	1000000.0	102.0	1000000.0
MP03137	PFC0700c	293	CAB11150	99.0248	RLFEESLGIR	10	923199.1	1000000.0	420.0	1000000.0
MP03137	PFC0700c	16	CAB11150	99.0370	PLFNNFYKR	9	11760.5	1000000.0	383.0	1000000.0
MP03137	PFC0700c	141	CAB11150	99.0371	YQNFQNADK	9	40121.5	1000000.0	637.4	1000000.0
MP03137	PFC0700c	184	CAB11150	99.0372	QMMNVNLQK	9	17662.1	1000000.0	1.4	1000000.0
MP03137	PFC0700c	222	CAB11150	99.0373	AVSEIQNNK	9	6991.0	1000000.0	3.1	1000000.0
MP03137	PFC0700c	236	CAB11150	99.0374	GTMYILLKK	9	986.2	1000000.0	0.5	1000000.0
MP03137	PFC0700c	260	CAB11150	99.0375	FISFYLINK	9	7376.0	1000000.0	12.2	1000000.0
MP03137	PFC0700c	264	CAB11150	99.0376	YLINKHWQR	9	39562.3	1000000.0	41.6	1000000.0
MP03137	PFC0700c	273	CAB11150	99.0377	ALKISQLQK	9	37884.8	1000000.0	5.1	1000000.0
MP03137	PFC0700c	282	CAB11150	99.0378	KINSNFLLK	9	5732.3	1000000.0	1.0	1000000.0

Table 5:
Pf-derived A3,11 supertype peptides scoring positive on PIC algorithm

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101 PIC	A*2402
12.t00018	Chromosome14	89		99.0249	QLKHFFNSNK	10	1000000.0	1000000.0	33.5	1000000.0
12.t00018	Chromosome14	615		99.0250	YVSMYIPFIK	10	301060.0	1000000.0	2.6	1000000.0
12.t00018	Chromosome14	671		99.0251	VLFYIYNMYH	10	900700.0	1000000.0	13.6	1000000.0
12.t00018	Chromosome14	705		99.0252	YTYIFFNYDK	10	742244.6	1000000.0	2.1	1000000.0
12.t00018	Chromosome14	1140		99.0253	SFFITYSYWK	10	1000000.0	1000000.0	5.7	1000000.0
12.t00018	Chromosome14	195		99.0379	STSNKHINR	9	6609.8	1000000.0	3.8	1000000.0
12.t00018	Chromosome14	687		99.0380	SQCNDYYIK	9	95255.3	1000000.0	6.3	1000000.0
12.t00018	Chromosome14	896		99.0381	SSIFYIKNK	9	41588.5	1000000.0	8.4	1000000.0
12.t00018	Chromosome14	1020		99.0382	LFFREKFLK	9	89243.3	1000000.0	14.3	1000000.0
12.t00018	Chromosome14	1160		99.0383	ILDNVSFLK	9	7621.1	1000000.0	21.0	1000000.0
mal_BU121g9.q1c1		10		99.0254	ILVLDIPGFK	10	1000000.0	1000000.0	55.0	1000000.0
mal_BU121g9.q1c1		45		99.0255	ETYGDSLVLH	10	453286.5	1000000.0	386.1	1000000.0
mal_BU121g9.q1c1		59		99.0256	EVGYFKRIFK	10	1000000.0	1000000.0	20.4	1000000.0
mal_BU121g9.q1c1		11		99.0384	LVLDIPGFK	9	13172.2	1000000.0	26.7	1000000.0
mal_BU121g9.q1c1		30		99.0385	GMLTVAGPR	9	54761.5	1000000.0	326.1	1000000.0
mal_BU121g9.q1c1		39		99.0386	SQTELFETY	9	6.7	1000000.0	254.2	1000000.0
mal_BU121g9.q1c1		48		99.0387	GDSLVLHAK	9	19504.9	1000000.0	306.8	1000000.0
mal_BU121g9.q1c1		50		99.0388	SLVLHAKER	9	133501.5	1000000.0	487.4	1000000.0
mal_BU121g9.q1c1		60		99.0389	VGYFKRIFK	9	44416.3	1000000.0	27.9	1000000.0
mal_BU121g9.q1c1		86		99.0390	NIYIYIYIY	9	40.2	1000000.0	322.7	1000000.0
mal_BU121g9.q1c1		88		99.0391	YIYIYIYIY	9	16.2	1000000.0	310.0	1000000.0
mal_9A57b11.q1t2		31		99.0257	SSFNCDIANK	10	1000000.0	1000000.0	8.4	1000000.0
mal_9A57b11.q1t2		49		99.0258	SMGVFCLKEK	10	1000000.0	1000000.0	24.6	1000000.0
mal_9A57b11.q1t2		119		99.0259	HIVKNRIYNK	10	1000000.0	1000000.0	51.7	1000000.0
mal_9A57b11.q1t2		128		99.0260	KLKLHKIIRK	10	1000000.0	1000000.0	64.9	1000000.0
mal_9A57b11.q1t2		165		99.0261	FIFDIFKYAR	10	1000000.0	1000000.0	148.8	1000000.0
mal_9A57b11.q1t2		202		99.0262	AQKALSNLHK	10	1000000.0	1000000.0	113.8	1000000.0
mal_9A57b11.q1t2		208		99.0263	NLHKSWLQYK	10	507559.4	1000000.0	199.6	1000000.0

Table 5:
Pf-derived A3,11 supertype peptides scoring positive on PIC algorithm

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101 PIC	A*2402
mal_9A57b11.q1t2		234		99.0264	YLPLFLMMEH	10	1000000.0	1000000.0	147.3	1000000.0
mal_9A57b11.q1t2		32		99.0392	SFNCDIANK	9	27329.1	1000000.0	35.4	1000000.0
mal_9A57b11.q1t2		62		99.0393	KINKKYNKK	9	40379.4	1000000.0	56.4	1000000.0
mal_9A57b11.q1t2		95		99.0394	ILNNKELFK	9	13663.7	1000000.0	29.6	1000000.0
mal_9A57b11.q1t2		120		99.0395	IVKNRIYNK	9	25949.5	1000000.0	17.8	1000000.0
mal_9A57b11.q1t2		154		99.0396	LINSKVFCY	9	6.1	1000000.0	113.8	1000000.0
mal_9A57b11.q1t2		183		99.0397	RQKEFYPIK	9	127059.4	1000000.0	38.7	1000000.0
mal_BL50e8.plca_5		9		99.0265	SFLVVLVFNK	10	1000000.0	1000000.0	33.6	1000000.0
mal_BL50e8.plca_5		152		99.0266	STYMTPSAIK	10	1000000.0	1000000.0	2.8	1000000.0
mal_BL50e8.plca_5		656		99.0267	KLYGEFTMNK	10	1000000.0	1000000.0	1.3	1000000.0
mal_BL50e8.plca_5		907		99.0268	GVYYIFVYLR	10	1000000.0	1000000.0	3.7	1000000.0
mal_BL50e8.plca_5		115		99.0398	SQYSNYFDY	9	11.0	1000000.0	15.2	1000000.0
mal_BL50e8.plca_5		361		99.0399	LFITYFQQK	9	90294.9	1000000.0	50.9	1000000.0
mal_BL50e8.plca_5		409		99.0400	ATSWDEYPK	9	44148.4	1000000.0	0.8	1000000.0
mal_BL50e8.plca_5		752		99.0401	ASFAAHENK	9	11256.9	1000000.0	0.2	1000000.0
mal_BL50e8.plca_5		780		99.0402	MLKADYFIR	9	35925.9	1000000.0	61.1	1000000.0
mal_BL50e8.plca_5		819		99.0403	VLNPVTIPK	9	14931.7	1000000.0	5.6	1000000.0
M13S8h6.plt_3		63		99.0269	VSYIFFMSFK	10	1000000.0	1000000.0	0.4	1000000.0
M13S8h6.plt_3		937		99.0270	MQKYFLHISK	10	1000000.0	1000000.0	37.5	1000000.0
M13S8h6.plt_3		25		99.0404	STFFFFLSR	9	3848.4	1000000.0	0.1	1000000.0
M13S8h6.plt_3		84		99.0405	LLLTFGVYY	9	22.7	1000000.0	157.5	1000000.0
M13S8h6.plt_3		157		99.0406	KFLFRYKQK	9	941796.8	1000000.0	16.1	1000000.0
M13S8h6.plt_3		394		99.0407	KVFIKGKGK	9	43309.1	1000000.0	3.8	1000000.0
M13S8h6.plt_3		1449		99.0408	ITYIWIILK	9	6990.4	1000000.0	1.6	1000000.0
M13S8h6.plt_3		1534		99.0409	KFFFFVFFY	9	51.8	1000000.0	3.5	2.2
M13S8h6.plt_3		1655		99.0410	KLLQKLISK	9	8661.9	1000000.0	53.4	1000000.0
M13S8h6.plt_3		1703		99.0411	ILNILKLAK	9	21447.1	1000000.0	55.0	1000000.0

Table 5:
Pf-derived A3,11 supertype peptides scoring positive on PIC algorithm

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101 PIC	A*2402
585.t00002	Chromosome11	193		99.0412	SQNNFSKIK	9	90378.2	1000000.0	9.1	1000000.0
585.t00002	Chromosome11	300		99.0413	SSLNIYNTK	9	46908.8	1000000.0	5.2	1000000.0
585.t00002	Chromosome11	529		99.0414	KLFNYKFFK	9	60297.3	1000000.0	1.0	1000000.0
585.t00002	Chromosome11	572		99.0415	LTFLSNIRK	9	13099.9	1000000.0	1.3	1000000.0
585.t00002	Chromosome11	616		99.0416	KFFYIFHYK	9	49030.6	1000000.0	0.2	1000000.0
585.t00002	Chromosome11	1415		99.0417	VTCSYFIIR	9	6831.4	1000000.0	16.8	1000000.0
585.t00002	Chromosome11	1487		99.0418	LTCAFKIYK	9	25752.8	1000000.0	0.3	1000000.0
585.t00002	Chromosome11	1508		99.0419	ILFILFFIK	9	9492.2	1000000.0	1.2	1000000.0
585.t00002	Chromosome11	1541		99.0420	NLYFFIHNR	9	13239.8	1000000.0	59.3	1000000.0
585.t00002	Chromosome11	1742		99.0421	IFLHYYFKK	9	118461.5	1000000.0	7.6	1000000.0
1223.t00015	mal_9A21f9.q1t_4	4294		99.0271	QVFFLQEMER	10	544655.4	1000000.0	27.6	1000000.0
1223.t00015	mal_9A21f9.q1t_4	272		99.0422	SFYKFEVEK	9	193104.9	1000000.0	16.1	1000000.0
1223.t00015	mal_9A21f9.q1t_4	325		99.0423	KTFREHFLK	9	17344.2	1000000.0	0.022	1000000.0
1223.t00015	mal_9A21f9.q1t_4	992		99.0424	VSNSSQLFK	9	13528.2	1000000.0	5.1	1000000.0
1223.t00015	mal_9A21f9.q1t_4	1397		99.0425	SLLNDVFPK	9	67376.3	1000000.0	1.2	1000000.0
1223.t00015	mal_9A21f9.q1t_4	1627		99.0426	KLFIFYLDK	9	25288.3	1000000.0	0.67	1000000.0
1223.t00015	mal_9A21f9.q1t_4	1664		99.0427	LLNSQIIQY	9	18.6	1000000.0	160.0	1000000.0
1223.t00015	mal_9A21f9.q1t_4	2115		99.0428	FQGFYFLDK	9	6204.2	1000000.0	44.3	1000000.0
1223.t00015	mal_9A21f9.q1t_4	2412		99.0429	NTFSFSWMK	9	16414.9	1000000.0	0.20	1000000.0
1223.t00015	mal_9A21f9.q1t_4	4500		99.0430	MFYNCPVYK	9	327575.1	1000000.0	10.3	1000000.0
599.t00001	Chromosome11	723		99.0272	NLLRHAIFYK	10	1000000.0	1000000.0	7.4	1000000.0
599.t00001	Chromosome11	1288		99.0273	SSYGYNIYFK	10	1000000.0	1000000.0	0.3	1000000.0
599.t00001	Chromosome11	1451		99.0274	RTYVNEYFLR	10	1000000.0	1000000.0	25.4	1000000.0
599.t00001	Chromosome11	16		99.0431	ILLTLVFQK	9	46527.3	1000000.0	2.9	1000000.0
599.t00001	Chromosome11	28		99.0432	CQNSLNYSK	9	38238.7	1000000.0	63.2	1000000.0
599.t00001	Chromosome11	211		99.0433	IVNNTELNK	9	9493.8	1000000.0	3.6	1000000.0
599.t00001	Chromosome11	776		99.0434	TLFSQNLFY	9	10.5	1000000.0	75.0	1000000.0
599.t00001	Chromosome11	1320		99.0435	TFYESVFTR	9	63945.9	1000000.0	27.9	1000000.0

Table 5:
Pf-derived A3,11 supertype peptides scoring positive on PIC algorithm

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101 PIC	A*2402
599.t00001	Chromosome11	1370		99.0436	YFFEEFFNK	9	19717.0	1000000.0	4.6	1000000.0
599.t00001	Chromosome11	1903		99.0437	TTQSNNIYK	9	20011.8	1000000.0	2.1	1000000.0
MP01072	M1045c5.p1c.C_6	1451		99.0275	SLFYFTSNGK	10	1000000.0	1000000.0	8.0	1000000.0
MP01072	M1045c5.p1c.C_6	46		99.0438	KLNYDNFEK	9	48445.0	1000000.0	3.4	1000000.0
MP01072	M1045c5.p1c.C_6	327		99.0439	ILCDDGIYR	9	19413.7	1000000.0	65.3	1000000.0
MP01072	M1045c5.p1c.C_6	359		99.0440	KVADVFLQH	9	6428.6	1000000.0	4.4	1000000.0
MP01072	M1045c5.p1c.C_6	419		99.0441	STSFLFLRK	9	2370.1	1000000.0	0.2	1000000.0
MP01072	M1045c5.p1c.C_6	421		99.0442	SFLFLRKQK	9	408258.6	1000000.0	12.7	1000000.0
MP01072	M1045c5.p1c.C_6	558		99.0443	SFFSSCENK	9	55537.2	1000000.0	17.7	1000000.0
MP01072	M1045c5.p1c.C_6	609		99.0444	AQSSYIYNK	9	18056.8	1000000.0	2.5	1000000.0
MP01072	M1045c5.p1c.C_6	1027		99.0445	MSAKYLYHK	9	5370.6	1000000.0	8.8	1000000.0
MP01072	M1045c5.p1c.C_6	1047		99.0446	TTLFSHFNK	9	10524.0	1000000.0	0.2	1000000.0
MP01072	M1045c5.p1c.C_6	1215		99.0447	SVYYNTMLR	9	9856.9	1000000.0	1.2	1000000.0
PIR2	T28161	1124		99.0276	VVNFLFELYK	10	408697.6	1000000.0	3.5	1000000.0
PIR2	T28161	1403		99.0277	TFFLWDRYKK	10	1000000.0	1000000.0	9.0	1000000.0
PIR2	T28161	108		99.0448	SVGACAPYR	9	59804.6	1000000.0	2.1	1000000.0
PIR2	T28161	204		99.0449	KQLEDNLRK	9	87893.1	1000000.0	16.9	1000000.0
PIR2	T28161	758		99.0450	KVASNMHHK	9	6948.7	1000000.0	1.6	1000000.0
PIR2	T28161	760		99.0451	ASNMHHKKK	9	32965.2	1000000.0	4.3	1000000.0
PIR2	T28161	838		99.0452	AGFISNTYK	9	154161.8	1000000.0	2.2	1000000.0
PIR2	T28161	965		99.0453	ILAFKEIYK	9	14274.5	1000000.0	12.6	1000000.0
PIR2	T28161	1879		99.0454	ALFKRWLEY	9	3.4	1000000.0	27.4	1000000.0
PIR2	T28161	2151		99.0455	AFTYFYLKK	9	40565.6	1000000.0	1.6	1000000.0
55.t00004	Chromosome14	483		99.0278	FFFSNVNNNK	10	409139.5	1000000.0	408.4	1000000.0
55.t00004	Chromosome14	564		99.0279	SQGKKNTYLK	10	1000000.0	1000000.0	13.0	1000000.0
55.t00004	Chromosome14	976		99.0280	VFNNSIILEK	10	1000000.0	1000000.0	372.4	1000000.0
55.t00004	Chromosome14	1338		99.0281	SVSEGYTSTY	10	67.8	1000000.0	33.5	1000000.0

Table 5:
Pf-derived A3,11 supertype peptides scoring positive on PIC algorithm

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101 PIC	A*2402
55.t00004	Chromosome14	229		99.0456	TSICKYWIK	9	8242.3	1000000.0	14.6	1000000.0
55.t00004	Chromosome14	263		99.0457	TTICKHWKK	9	4558.7	1000000.0	1.7	1000000.0
55.t00004	Chromosome14	537		99.0458	KVTNVHIYK	9	41321.8	1000000.0	0.2	1000000.0
55.t00004	Chromosome14	866		99.0459	ITNMNNINR	9	5371.8	1000000.0	37.6	1000000.0
55.t00004	Chromosome14	909		99.0460	MLNIYKINK	9	17179.3	1000000.0	13.6	1000000.0
55.t00004	Chromosome14	1030		99.0461	IINSYIDYK	9	84561.6	1000000.0	2.0	1000000.0
55.t00004	Chromosome14	1141		99.0462	NLYTYVVNK	9	45076.1	1000000.0	54.8	1000000.0
55.t00004	Chromosome14	1665		99.0463	KMIYSIFIK	9	42191.9	1000000.0	4.1	1000000.0
13.t00011	Chromosome14	8		99.0282	ISMDKSLFFK	10	1000000.0	1000000.0	16.7	1000000.0
13.t00011	Chromosome14	47		99.0283	TVFLDYVKGK	10	1000000.0	1000000.0	7.8	1000000.0
13.t00011	Chromosome14	59		99.0284	DVYKETNMNR	10	1000000.0	1000000.0	64.9	1000000.0
13.t00011	Chromosome14	117		99.0285	KLKKSTICNK	10	1000000.0	1000000.0	59.9	1000000.0
13.t00011	Chromosome14	9		99.0464	SMDKSLFFK	9	4208.2	1000000.0	3.5	1000000.0
13.t00011	Chromosome14	12		99.0465	KSLFFKSLK	9	64105.1	1000000.0	17.4	1000000.0
13.t00011	Chromosome14	48		99.0466	VFLDYVKGK	9	347222.4	1000000.0	216.7	1000000.0
13.t00011	Chromosome14	93		99.0467	KVKRFRVFK	9	52490.3	1000000.0	3.3	1000000.0
13.t00011	Chromosome14	104		99.0468	SFFIDEVKK	9	352606.0	1000000.0	37.8	1000000.0
13.t00011	Chromosome14	112		99.0469	KIYENKLKK	9	30696.4	1000000.0	14.5	1000000.0
37.t00002	Chromosome14	13		99.0286	ALTYMYCVYY	10	249.1	1000000.0	112.8	1000000.0
37.t00002	Chromosome14	31		99.0287	SQISIFCNLR	10	1000000.0	1000000.0	226.6	1000000.0
37.t00002	Chromosome14	32		99.0288	QISIFCNLRR	10	301919.5	1000000.0	80.8	1000000.0
37.t00002	Chromosome14	62		99.0289	VCNNETYYNK	10	1000000.0	1000000.0	186.8	1000000.0
37.t00002	Chromosome14	71		99.0290	KAHEENDKVK	10	1000000.0	1000000.0	956.7	1000000.0
37.t00002	Chromosome14	13		99.0470	ALTYMYCVY	9	9.1	1000000.0	279.6	1000000.0
37.t00002	Chromosome14	32		99.0471	QISIFCNLR	9	26897.2	1000000.0	855.0	1000000.0
37.t00002	Chromosome14	33		99.0472	ISIFCNLRR	9	37287.9	1000000.0	255.9	1000000.0
37.t00002	Chromosome14	61		99.0473	NVCNNETYY	9	25.3	1000000.0	514.8	1000000.0

Table 5:
Pf-derived A3,11 supertype peptides scoring positive on PIC algorithm

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101 PIC	A*2402
674.t00001	Chromosome11	90		99.0291	LVEFIFLLLK	10	304423.1	1000000.0	13.7	1000000.0
674.t00001	Chromosome11	218		99.0292	SVFYNKEIIK	10	993500.3	1000000.0	4.5	1000000.0
674.t00001	Chromosome11	867		99.0293	SLKDFDMLLY	10	199.3	1000000.0	214.4	1000000.0
674.t00001	Chromosome11	64		99.0474	NVNDRFVEK	9	13728.8	1000000.0	11.8	1000000.0
674.t00001	Chromosome11	662		99.0475	TLSNSLPQK	9	36834.4	1000000.0	47.0	1000000.0
674.t00001	Chromosome11	673		99.0476	YQINNFIHK	9	12103.7	1000000.0	59.8	1000000.0
674.t00001	Chromosome11	689		99.0477	NLTINNFQK	9	59129.2	1000000.0	40.3	1000000.0
674.t00001	Chromosome11	1035		99.0478	KFNRDMLQK	9	254779.4	1000000.0	1.9	1000000.0
674.t00001	Chromosome11	1126		99.0479	NQSDFLLLK	9	8015.9	1000000.0	15.2	1000000.0
674.t00001	Chromosome11	1256		99.0480	SFHHFNIDK	9	178323.3	1000000.0	26.2	1000000.0
674.t00001	Chromosome11	1288		99.0481	KSKELLLQK	9	27230.7	1000000.0	4.4	1000000.0

Table 6:
Pf-derived 15mer peptides with nonamer core sequences scoring DR1 PIC <4nM

Antigen	Addn Source info	Position	Peptide No.	Sequence	AA	DR1 PIC
331.t00003	Chromosome10	182	100.0001	LSHFKKNFILQNNEE	15	0.447
331.t00003	Chromosome10	365	100.0002	TTFLSALKLLKIAQY	15	0.400
331.t00003	Chromosome10	428	100.0003	NNKLSKNLSQLVHFY	15	0.130
331.t00003	Chromosome10	617	100.0004	KIYMFGGFSKGVRNN	15	0.061
331.t00003	Chromosome10	894	100.0005	DDMIGMPNLSSTVVC	15	0.337
331.t00003	Chromosome10	987	100.0006	TFTFQNMYVRSKVVS	15	0.400
331.t00003	Chromosome10	1365	100.0007	KYEIIGNILIFHYKY	15	0.435
331.t00003	Chromosome10	1601	100.0008	KERMKNMYIVSNNDD	15	0.013
331.t00003	Chromosome10	1656	100.0009	GVGYFTLPLLKCIEA	15	0.302
331.t00003	Chromosome10	1725	100.0010	HRIILGLLPHSQPAW	15	0.167
Chr12Contig18	18.000811	13	100.0011	HFFLFLLYILFLVKM	15	1.826
Chr12Contig18	18.000811	16	100.0012	LFLLYILFLVKMNAL	15	0.593
Chr12Contig18	18.000811	21	100.0013	ILFLVKMNALRRLPV	15	0.035
Chr12Contig18	18.000811	27	100.0014	MNALRRLPVICSFLV	15	3.206
Chr12Contig18	18.000811	79	100.0015	SAFLESQSMNKIGDD	15	3.392
Chr12Contig18	18.000811	132	100.0016	LKELIKVGLPSFENL	15	0.785
Chr12Contig18	18.000811	143	100.0017	FENLVAENVKPPKVD	15	0.854
Chr12Contig18	18.000811	148	100.0018	AENVKPPKVDPATYG	15	3.392
Chr12Contig18	18.000811	158	100.0019	PATYGIIVPVLTSLF	15	0.221
Chr12Contig18	18.000811	161	100.0020	YGIIVPVLTSLFNKV	15	0.956
MY924Fe3.pltl		1015	100.0021	SVDLQIKISMKVLNS	15	0.103
MY924Fe3.pltl		1021	100.0022	KISMKVLNSMFHIIM	15	0.234
MY924Fe3.pltl		1076	100.0023	KDVVQIQTVLLSLGF	15	0.066
MY924Fe3.pltl		1331	100.0024	SQIIIILPSILENIL	15	0.092
MY924Fe3.pltl		1526	100.0025	MHSVKEMIVYLIQNN	15	0.262
MY924Fe3.pltl		1703	100.0026	TINLINELMKRQHDK	15	0.192
MY924Fe3.pltl		1746	100.0027	REMLLKMKSMSRNQR	15	0.130
MY924Fe3.pltl		1878	100.0028	RSIIFAGHTIELNSL	15	0.248
MY924Fe3.pltl		1890	100.0029	NSLMFKQTSGRAGRR	15	0.061

Table 6:
Pf-derived 15mer peptides with nonamer core sequences scoring DR1 PIC <4nM

Antigen	Addn Source info	Position	Peptide No.	Sequence	AA	DR1	PIC
MY924Fe3.pltl		2201	100.0030	NLIITYLLIKKVLHN	15	0.162	
MP03001	MAL3P2.11	1	100.0031	MRKLAILSVSSFLFV	15	2.786	
MP03001	MAL3P2.11	36	100.0032	ELNYDNAGTNLYNEL	15	1.040	
MP03001	MAL3P2.11	342	100.0033	QVRIKPGSANKPKDE	15	0.460	
1369.t00001	Chromosome 11	28	100.0034	LLKIWKNYMKIMNHL	15	0.328	
1369.t00001	Chromosome 11	43	100.0035	MTLYQIQVMKRNQKQ	15	0.056	
1369.t00001	Chromosome 11	57	100.0036	QKQVQMMIMIKFMGV	15	0.016	
1369.t00001	Chromosome 11	63	100.0037	MIMIKFMGVIYIMII	15	0.545	
1369.t00001	Chromosome 11	70	100.0038	GVIYIMIISKKMMRK	15	0.076	
1369.t00001	Chromosome 11	285	100.0039	LYYLFNQHIKKELYH	15	0.742	
1369.t00001	Chromosome 11	299	100.0040	HFNMLKNKMQSSFFM	15	0.560	
1369.t00001	Chromosome 11	353	100.0041	XDIYQKLYIKQEEQK	15	0.807	
1369.t00001	Chromosome 11	366	100.0042	QKKYIYNLIMNTQNK	15	0.167	
1369.t00001	Chromosome 11	381	100.0043	YEALIKLLPFSKRIR	15	0.701	
699.t00001	Chromosome 11	565	100.0044	NIHFAVLFLTLTVYP	15	0.347	
699.t00001	Chromosome 11	569	100.0045	AVLFLTLTVYPINNF	15	0.255	
699.t00001	Chromosome 11	623	100.0046	KLLYKMNYLKQDINN	15	0.545	
699.t00001	Chromosome 11	744	100.0047	KKEFKNSLILLNLYN	15	0.576	
699.t00001	Chromosome 11	773	100.0048	YLSFKILNTLLYNHI	15	0.234	
699.t00001	Chromosome 11	866	100.0049	IYILINHVIIPSLFY	15	0.400	
699.t00001	Chromosome 11	875	100.0050	IPSLFYLYMNFLKFI	15	0.347	
699.t00001	Chromosome 11	929	100.0051	KYLIILLYIFKLIEY	15	0.701	
699.t00001	Chromosome 11	978	100.0052	FIFMQNNQTKLAEMK	15	0.039	
699.t00001	Chromosome 11	1032	100.0053	LFIYIWLHLIIIFIF	15	0.423	
mal_4T2c4.pltl		15	100.0054	ILLIRPMLVKLRPKL	15	0.221	
mal_4T2c4.pltl		19	100.0055	RPMLVKLRPKLVKLR	15	0.083	
mal_4T2c4.pltl		26	100.0056	RPKLVKLRPMLVKLG	15	0.010	
mal_4T2c4.pltl		33	100.0057	RPMLVKLGPILVKLR	15	0.004	
mal_4T2c4.pltl		40	100.0058	GPILVKLRPMLVKLR	15	0.010	

Table 6:
Pf-derived 15mer peptides with nonamer core sequences scoring DR1 PIC <4nM

Antigen	Addn Source info	Position	Peptide No.	Sequence	AA	DR1	PIC
mal_4T2c4.p1t1		47	100.0059	RPMLVKLRPMLAKLR	15		0.016
mal_4T2c4.p1t1		54	100.0060	RPMLAKLRPMLAKLR	15		0.027
mal_4T2c4.p1t1		61	100.0061	RPMLAKLRPKLVKLR	15		0.137
mal_4T2c4.p1t1		68	100.0062	RPKLVKLRPKLVKLR	15		0.083
mal_4T2c4.p1t1		75	100.0063	RPKLVKLRPISVNAK	15		0.076
M13Hg2.q1t3		89	100.0064	ILEMKPNILLSRFIF	15		0.742
M13Hg2.q1t3		122	100.0065	NISINNAFSLPVNIY	15		0.663
M13Hg2.q1t3		163	100.0066	YFNIIQQKIQSNFLL	15		0.487
M13Hg2.q1t3		281	100.0067	ISTFIKNNINHQENN	15		0.682
M13Hg2.q1t3		442	100.0068	LKNMDGNILIKDFIQ	15		0.378
M13Hg2.q1t3		488	100.0069	IEFYNINMAKKVMNN	15		0.285
M13Hg2.q1t3		492	100.0070	NINMAKKVMNNMEKN	15		0.145
M13Hg2.q1t3		558	100.0071	FVNYFEAVVHMNIHC	15		0.831
M13Hg2.q1t3		691	100.0072	NNNIINGHMLEQKLS	15		0.123
M13Hg2.q1t3		869	100.0073	NNDMKKGYTNVSNNS	15		0.162
Mal_5L10c4.q1t6		154	100.0074	NNEFFGYPLQFVCET	15		0.255
Mal_5L10c4.q1t6		336	100.0075	FFIIKNVGVHKITYY	15		0.388
Mal_5L10c4.q1t6		1090	100.0076	KIEYISMLSPTINEI	15		0.113
Mal_5L10c4.q1t6		1101	100.0077	INEIKTLNTILTIPL	15		0.018
Mal_5L10c4.q1t6		1107	100.0078	LNTILTIPLIKMNEY	15		0.042
Mal_5L10c4.q1t6		1264	100.0079	HKLFINKLMTSNIRK	15		0.203
Mal_5L10c4.q1t6		1289	100.0080	QNRFRNQLLYLTKIA	15		0.050
Mal_5L10c4.q1t6		1609	100.0081	IKKIKTPLILPIDPN	15		0.035
Mal_5L10c4.q1t6		1888	100.0082	QDHLVIQIIYVMDNI	15		0.133
Mal_5L10c4.q1t6		2031	100.0083	IEAMGGAHSIGYEQF	15		0.068
571.t00003	Chromosome11	33	100.0084	FDDFKINYSYKTKNH	15		0.182
571.t00003	Chromosome11	462	100.0085	ITDLNNMNVNQSNMK	15		0.500
571.t00003	Chromosome11	960	100.0086	TNNFNNNVMMLMNTS	15		0.007
571.t00003	Chromosome11	1124	100.0087	EQNVAQNVAQNVAQN	15		0.460

Table 6:
Pf-derived 15mer peptides with nonamer core sequences scoring DR1 PIC <4nM

Antigen	Addn Source info	Position	Peptide No.	Sequence	AA	DR1	PIC
571.t00003	Chromosome11	1128	100.0088	AQNVAQNVAQNVEQN	15		0.460
571.t00003	Chromosome11	1550	100.0089	SNKFMTPTTLKEKYQ	15		0.255
571.t00003	Chromosome11	1941	100.0090	NIHMINDVATKLNQH	15		0.285
571.t00003	Chromosome11	2112	100.0091	HIHMMNQQIQKETNT	15		0.576
571.t00003	Chromosome11	2255	100.0092	NNVFQQPLSYSNGSE	15		0.347
571.t00003	Chromosome11	2738	100.0093	NNTINMNGMNKTESI	15		0.198
MP03072	PFC0450w	5	100.0094	LNILILIDAASVAFL	15		0.722
MP03072	PFC0450w	8	100.0095	LILIDAASVAFLLIT	15		1.340
MP03072	PFC0450w	17	100.0096	AFLLITFLMINLNEE	15		1.197
MP03072	PFC0450w	44	100.0097	KKALVVAIILYVIFL	15		0.302
MP03072	PFC0450w	48	100.0098	VVAIILYVIFLVLLF	15		0.609
MP03072	PFC0450w	52	100.0099	ILYVIFLVLLFIYKA	15		0.831
MP03072	PFC0450w	55	100.0100	VIFLVLLFIYKAYKN	15		0.956
MP03072	PFC0450w	58	100.0101	LVLLFIYKAYKNKRK	15		4.016
MP03072	PFC0450w	76	100.0102	NFFMKKRNAPKYVQL	15		0.593
MP03072	PFC0450w	85	100.0103	PKYVQLASTYLSASD	15		2.865
45.t00001	Chromosome14	2	100.0104	ENEYATGAVRPFQAA	15		0.722
45.t00001	Chromosome14	27	100.0105	NYELSKKAVIFTPIY	15		1.197
45.t00001	Chromosome14	108	100.0106	QKILIKIPVTKNIIT	15		0.085
45.t00001	Chromosome14	156	100.0107	KCLVISQVSNSDSYK	15		2.044
45.t00001	Chromosome14	202	100.0108	SKIMKLPKLPISNGK	15		0.742
45.t00001	Chromosome14	220	100.0109	FIHFFTWGTMFVPKY	15		0.026
45.t00001	Chromosome14	242	100.0110	LCNFKKNIIALLIIP	15		0.203
45.t00001	Chromosome14	246	100.0111	KKNIIALLIIPPKIH	15		0.010
45.t00001	Chromosome14	251	100.0112	ALLIIPPKIHISIEL	15		1.267
45.t00001	Chromosome14	274	100.0113	SMEYKKDFLITARKP	15		1.826
MP03137	PFC0700c	7	100.0114	KSKFNILSSPLFNNF	15		1.987
MP03137	PFC0700c	173	100.0115	FKKLKNHVLFLQMMN	15		0.785
MP03137	PFC0700c	177	100.0116	KNHVLFLQMMNVNLQ	15		0.095

Table 6:
Pf-derived 15mer peptides with nonamer core sequences scoring DR1 PIC <4nM

Antigen	Addn Source info	Position	Peptide No.	Sequence	AA	DR1	PIC
MP03137	PFC0700c	180	100.0117	VLFLQMMNVNLQKQL	15	0.068	
MP03137	PFC0700c	187	100.0118	NVNLQKQLLTNHLIN	15	0.956	
MP03137	PFC0700c	191	100.0119	QKQLLTNHLINTPKI	15	1.132	
MP03137	PFC0700c	197	100.0120	NHLINTPKIMPHHII	15	0.576	
MP03137	PFC0700c	239	100.0121	YILLKKILSSRFNQM	15	1.100	
MP03137	PFC0700c	250	100.0122	FNQMIFVSSIFISFY	15	2.420	
12.t00018	Chromosome14	36	100.0123	CNILKENNTYKQKKH	15	4.016	
12.t00018	Chromosome14	133	100.0124	TNELKKMDTKKDVHM	15	1.011	
12.t00018	Chromosome14	504	100.0125	EVKFILHMTLLTLYK	15	0.269	
12.t00018	Chromosome14	542	100.0126	KYNFLNIYASLRNEY	15	0.328	
12.t00018	Chromosome14	583	100.0127	TRCFKNSYPKKVWKK	15	0.293	
12.t00018	Chromosome14	612	100.0128	NNLYVSMYIPFIKKF	15	0.411	
12.t00018	Chromosome14	1000	100.0129	EAKFKIERLLKSSYK	15	3.298	
12.t00018	Chromosome14	1057	100.0130	KIYILNNNLLIVHLS	15	1.543	
12.t00018	Chromosome14	1184	100.0131	KCSFDKTNPIQQSGK	15	2.044	
12.t00018	Chromosome14	1212	100.0132	TGIFNMPNLVQINNY	15	0.078	
mal_BU121g9.q1c1		29	100.0133	EGMLTVAGPRSQTEL	15	3.298	
mal_9A57b11.q1t2		3	100.0134	KQNIKYTQIISIDNI	15	2.633	
mal_9A57b11.q1t2		18	100.0135	LNKIADPILIGFSSS	15	0.929	
mal_9A57b11.q1t2		123	100.0136	NRIYNKLKLHKIIRK	15	1.267	
mal_9A57b11.q1t2		194	100.0137	NNEYGILNAQKALSN	15	0.098	
mal_9A57b11.q1t2		197	100.0138	YGILNAQKALSNLHK	15	0.141	
mal_9A57b11.q1t2		229	100.0139	KIFVKYLPLFLMMEH	15	0.042	
mal_9A57b11.q1t2		236	100.0140	PLFLMMEHSFLNCHK	15	3.031	
mal_BL50e8.p1ca_5		1	100.0141	MEGFVALLSFLVVLV	15	0.004	
mal_BL50e8.p1ca_5		100	100.0142	VDGMKIGHPISVALG	15	0.010	
mal_BL50e8.p1ca_5		151	100.0143	GSTYMTPSAIKIKVP	15	0.057	
mal_BL50e8.p1ca_5		189	100.0144	NNLFIYNWVLQTSSP	15	0.560	
mal_BL50e8.p1ca_5		347	100.0145	EKILIRALLSLDFSL	15	0.722	

Table 6:
Pf-derived 15mer peptides with nonamer core sequences scoring DR1 PIC <4nM

Antigen	Addn Source info	Position	Peptide No.	Sequence	AA	DR1	PIC
mal_BL50e8.plca_5		437	100.0146	HPVYPTAPAVAFPAG	15	0.187	
mal_BL50e8.plca_5		585	100.0147	EVYYFPGKVTRVRAK	15	0.357	
mal_BL50e8.plca_5		606	100.0148	EDKLVKIYISLLSSD	15	0.423	
mal_BL50e8.plca_5		685	100.0149	IERYVGLGSFHFYLY	15	0.423	
mal_BL50e8.plca_5		816	100.0150	CFQVLNPVTIPKYCI	15	0.285	
M13S8h6.plt_3		68	100.0151	FMSFKILEALLVCIS	15	0.006	
M13S8h6.plt_3		127	100.0152	KQIVIFLISLLSFTL	15	0.473	
M13S8h6.plt_3		169	100.0153	AKQIEILHTMLPNFL	15	0.095	
M13S8h6.plt_3		218	100.0154	IDDFQNMVSTLQPHV	15	0.034	
M13S8h6.plt_3		285	100.0155	KCAIKLAIAQLSAKY	15	0.130	
M13S8h6.plt_3		343	100.0156	IGSVKPQYALFGDTV	15	0.228	
M13S8h6.plt_3		871	100.0157	KIYIKKKRLLQMNNY	15	0.411	
M13S8h6.plt_3		1350	100.0158	KKLLKKLTSNLQLNK	15	0.076	
M13S8h6.plt_3		1602	100.0159	QDFLTKILPRQVLEE	15	0.241	
M13S8h6.plt_3		1754	100.0160	MWGLDVLIANKIESN	15	0.423	
585.t00002	Chromosome11	5	100.0161	FFILFYFYVMSTYTF	15	0.500	
585.t00002	Chromosome11	16	100.0162	TYTFCFLPVLQTQLG	15	0.515	
585.t00002	Chromosome11	349	100.0163	KKKYKNKKMPKTIDG	15	0.473	
585.t00002	Chromosome11	487	100.0164	GRAIIPLFLILNTYK	15	0.269	
585.t00002	Chromosome11	562	100.0165	KIIFKRNPLFLTFLS	15	0.367	
585.t00002	Chromosome11	643	100.0166	WLFFFDLVVLSPFSL	15	0.500	
585.t00002	Chromosome11	774	100.0167	KNIIKGKNMMTRGGG	15	0.106	
585.t00002	Chromosome11	796	100.0168	KMFIKGDTVMKANII	15	0.038	
585.t00002	Chromosome11	1093	100.0169	VGSYKLMISQEAEFE	15	0.487	
585.t00002	Chromosome11	1344	100.0170	LNRFITLITWTQHVS	15	0.095	
1223.t00015	mal_9A21f9.qlt_4	1070	100.0171	RTKYETLVTIHVHQR	15	0.087	
1223.t00015	mal_9A21f9.qlt_4	1162	100.0172	GLCYGGAPAGPAGTG	15	0.059	
1223.t00015	mal_9A21f9.qlt_4	1654	100.0173	DSILILQTINLLNSQ	15	0.177	
1223.t00015	mal_9A21f9.qlt_4	2461	100.0174	KHLIIINRVMQTPNG	15	0.043	

Table 6:
Pf-derived 15mer peptides with nonamer core sequences scoring DR1 PIC <4nM

Antigen	Addn Source info	Position	Peptide No.	Sequence	AA	DR1	PIC
1223.t00015	mal_9A21f9.q1t_4	2779	100.0175	IDLYKQMYVKKYDEI	15		0.158
1223.t00015	mal_9A21f9.q1t_4	2878	100.0176	DKDLKAALPYLHEAE	15		0.103
1223.t00015	mal_9A21f9.q1t_4	2985	100.0177	TIELLKPYIQSTFFK	15		0.145
1223.t00015	mal_9A21f9.q1t_4	2995	100.0178	STFFKTQIAKKASVA	15		0.002
1223.t00015	mal_9A21f9.q1t_4	3014	100.0179	CKWVGAMAMYNQASK	15		0.145
1223.t00015	mal_9A21f9.q1t_4	3019	100.0180	AMAMYNQASKIVKPK	15		0.116
599.t00001	Chromosome11	12	100.0181	INFFILLTLVFQKYS	15		0.177
599.t00001	Chromosome11	364	100.0182	NNNLGIPTLIKKEVH	15		0.234
599.t00001	Chromosome11	519	100.0183	EEDIKNAYLPENKNF	15		0.435
599.t00001	Chromosome11	1074	100.0184	INVFIKEISKLFDHD	15		0.529
599.t00001	Chromosome11	1414	100.0185	DKSLKIMYSLFNKYT	15		0.098
599.t00001	Chromosome11	1463	100.0186	VVIFIYGNIIISDLK	15		0.645
599.t00001	Chromosome11	1621	100.0187	CESFISKVTNKVIKK	15		0.215
599.t00001	Chromosome11	1740	100.0188	ICTFVKYITFQLLNI	15		0.854
599.t00001	Chromosome11	1767	100.0189	KEHYIMNNTIFTFNQ	15		0.141
599.t00001	Chromosome11	1892	100.0190	KKKYKYIPSNGTTQS	15		0.500
M1045c5.p1c.C_6		53	100.0191	EKSLGILGSIQNAYL	15		0.085
M1045c5.p1c.C_6		59	100.0192	LGSIQNAYLYKSIFK	15		0.388
M1045c5.p1c.C_6		588	100.0193	SCIMNNMIVTKESNE	15		0.473
M1045c5.p1c.C_6		1040	100.0194	KDFMKNNTTLFSHFN	15		0.241
M1045c5.p1c.C_6		1136	100.0195	MLYLIRNILMSIEDY	15		0.435
M1045c5.p1c.C_6		1229	100.0196	KKKYIKLNIFKNIIL	15		0.378
M1045c5.p1c.C_6		1350	100.0197	RWDLVMNMMIGIRIS	15		0.054
M1045c5.p1c.C_6		1380	100.0198	HKDVIQLPTSNAQHK	15		0.167
M1045c5.p1c.C_6		1393	100.0199	HKVIFKNYAPIIFKN	15		0.262
M1045c5.p1c.C_6		1430	100.0200	SNMVLGNLSTLSELL	15		0.423
PIR2	T28161	46	100.0201	AKFYNGGEIMQPNSK	15		0.153
PIR2	T28161	319	100.0202	KRNLKLQNAIKNCRG	15		0.043
PIR2	T28161	1072	100.0203	HVKIIKNLLIHGKEQ	15		0.302

Table 6:
Pf-derived 15mer peptides with nonamer core sequences scoring DR1 PIC <4nM

Antigen	Addn Source info	Position	Peptide No.	Sequence	AA	DR1	PIC
PIR2	T28161	1093	100.0204	KYKLLYLQAQTTAAN	15	0.141	
PIR2	T28161	1096	100.0205	LLYLQAQTTAANGGP	15	0.047	
PIR2	T28161	1589	100.0206	SPKIVVPAPKPTTTF	15	0.119	
PIR2	T28161	1951	100.0207	FVDLIRQIAATIDKG	15	0.047	
PIR2	T28161	2065	100.0208	QERLVKNPLVQPTLK	15	0.028	
PIR2	T28161	2129	100.0209	HPAVIPALVTSTLAW	15	0.072	
PIR2	T28161	2419	100.0210	NELFGTNHVKQTSIH	15	0.098	
55.t00004	Chromosome14	81	100.0211	NNEFVVAQLYELNNY	15	1.340	
55.t00004	Chromosome14	117	100.0212	DNNMKKYLIQKCGKK	15	1.776	
55.t00004	Chromosome14	218	100.0213	SCSIIKYELRKTSIC	15	1.878	
55.t00004	Chromosome14	385	100.0214	RNHMDKPPPHNINNN	15	0.228	
55.t00004	Chromosome14	613	100.0215	NNNLIFQNSRFMDHT	15	0.423	
55.t00004	Chromosome14	754	100.0216	THDIIKNVSNNMKRF	15	0.357	
55.t00004	Chromosome14	904	100.0217	FKNVDMLNIYKINKD	15	1.987	
55.t00004	Chromosome14	1136	100.0218	MKDVINLYTYVVNKK	15	0.092	
55.t00004	Chromosome14	1364	100.0219	GMYILPQYVTRECIN	15	1.500	
55.t00004	Chromosome14	1510	100.0220	GDDVIYEETKKTDNI	15	1.587	
13.t00011	Chromosome14	16	100.0221	FKSLKNNNMLESTGI	15	1.587	
13.t00011	Chromosome14	49	100.0222	FLDYVKGKMMDVYKE	15	0.126	
13.t00011	Chromosome14	84	100.0223	TYNYLTPTLKVKRFR	15	3.589	
37.t00002	Chromosome14	50	100.0224	NDLIDQNIVYLNVCN	15	2.560	
674.t00001	Chromosome11	30	100.0225	LKKLKKILLNLDVLI	15	0.742	
674.t00001	Chromosome11	54	100.0226	NENFDMELLNNVNDR	15	1.378	
674.t00001	Chromosome11	124	100.0227	NCPIKNEVTTLIQKI	15	0.367	
674.t00001	Chromosome11	296	100.0228	EKNMTSQKSITSEKN	15	0.854	
674.t00001	Chromosome11	577	100.0229	NSNFKEQHLLFCNNL	15	1.418	
674.t00001	Chromosome11	752	100.0230	NNNIKTHIANFNIIH	15	1.040	
674.t00001	Chromosome11	986	100.0231	NNLYKTYEMIQGDND	15	0.956	
674.t00001	Chromosome11	1093	100.0232	NDNYINNNIYLNKAN	15	1.340	

Table 6:
Pf-derived 15mer peptides with nonamer core sequences scoring DR1 PIC <4nM

Antigen	Addn Source info	Position	Peptide No.	Sequence	AA	DR1	PIC
674.t00001	Chromosome11	1353	100.0233	FLQYRIPHMNNNGNI	15	0.983	
674.t00001	Chromosome11	1432	100.0234	VDIFCKIHALKNENK	15	0.854	

Claims

1. An isolated and/or purified polynucleotide sequence comprising:

a) a polynucleotide sequence encoding: 1) a polypeptide sequence selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27; or 2) a polypeptide as set forth in Tables 2, 3, 4, 5, or 6;

b) a complementary polynucleotide sequence to: 1) a polynucleotide sequence encoding a polypeptide sequence selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27; or 2) a polynucleotide sequence encoding a polypeptide sequence as set forth in Tables 2, 3, 4, 5, or 6

c) a polynucleotide sequence having at least about 20% to 99.99% identity to a polynucleotide sequence of 1(a) or 1(b);

d) a fragment of a polynucleotide sequence according to 1(a) or 1(b);

e) a polynucleotide sequence encoding a variant of: 1) a polypeptide selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27; or 2) a polypeptide as set forth in Tables 2, 3, 4, 5, or 6;

g) a polynucleotide sequence encoding a polypeptide fragment of a polypeptide selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27, wherein the fragment has substantially the same serologic reactivity as the native polypeptide and substantially the same T-cell reactivity as the native polypeptide or fragment;

h) a polynucleotide sequence encoding a fragment of a variant polypeptide of a polypeptide selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27, wherein the fragment of the variant polypeptide has substantially the same serologic activity as the native polypeptide or substantially the same T-cell reactivity as the native polypeptide or fragment; or

i) a polynucleotide sequence encoding a multi-epitope construct.

2. A primer or detection probe for hybridization with a target sequence or the amplicon generated from a target sequence comprising a sequence of at least 8, 9, 10, 11,

12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 consecutive nucleotides of the polynucleotide sequences according to claim 1.

3. The isolated polynucleotide according to claims 1 or 2 further comprising a label.

4. The isolated polynucleotide according to claim 3, wherein said label is a: 1) radioactive label, 2) enzyme label, 3) chemiluminescent label, 4) fluorescent label, or 5) magnetic label.

5. The method of detecting *P. falciparum* in biological samples comprising contacting a biological sample with isolated polynucleotides of claim 1, 2, 3, or 4 and detecting the hybridization of said isolated polynucleotides with nucleic acids contained in said sample.

6. A DNA chip comprising polynucleotide sequences according to claims 1, 2, 3 or 4.

7. An isolated polynucleotide sequence according to claim 1 or 2, further comprising regulatory sequences.

8. The isolated polynucleotide sequence according to claim 7, wherein said regulatory sequences are promoters, enhancer elements, or termination sequences that are operably linked to said polynucleotide.

9. A vector comprising a promoter operably linked to a nucleic acid sequence according to claim 1.

10. The vector according to claim 9, wherein said vector contains one or more origins of replication.

11. The vector according to claim 10, wherein said vector contains one or more selectable markers.

12. The vector according to claim 9, wherein said vector contains one or more selectable markers.

13. The vector according to claim 9, wherein said vector is a vaccine vector or a viral vector.

14. A vector comprising a promoter operably linked to a nucleic acid sequence according to claim 2.

15. The vector according to claim 14, wherein said vector contains one or more origins of replication.

16. The vector according to claim 15, wherein said vector contains one or more selectable markers.

17. The vector according to claim 14, wherein said vector contains one or more selectable markers.

18. The vector according to claim 14, wherein said vector is a vaccine vector or a viral vector.

19. A host cell transformed by: 1) a vector according claim 9, 10, 11, 12, 13, 14, 15, 16, 17 or 18; or 2) a polynucleotide according to claim 1, 2, or 7.

20. A composition comprising a pharmaceutically acceptable carrier and a polynucleotide according to claim 1, 2, 7, 9, 10, 11, 12, 13, 14, 15, 16, 17 or 18.

21. A method of inducing an immune response in an individual comprising the administration of a composition according to claim 20 in an amount sufficient to induce an immune response.

22. An isolated polypeptide comprising:

a) SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27;

b) a polypeptide as set forth in Tables 2, 3, 4, 5, or 6;

c) a fragment of a polypeptide or a variant polypeptide of: a) a polypeptide set forth in SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27; or b) a polypeptide as set forth in Tables 2, 3, 4, 5, or 6, wherein said fragment or variant has substantially the same serologic reactivity or substantially the same T-cell reactivity as the native polypeptide;

d) a variant polypeptide having at least about 20% to 99.99% identity to a polypeptide provided in Table 2, 3, 4, 5, or 6 or selected from the group consisting of SEQ ID NO: NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27;

e) a polypeptide epitope as set forth in Table 2, 3, 4, 5, or 6; or

f) a multi-epitope construct: 1) comprising at least one epitope set forth in Table 2, 3, 4, 5, or 6; 2) comprising a polypeptide selected from the group consisting of SEQ ID NO: NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27 and at least one epitope set forth in Table 2, 3, 4, 5, or 6; or 3) comprising and at least one epitope set forth in Table 2, 3, 4, 5, or 6 and one or more polypeptide selected from the group consisting of SEQ ID NO: NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27.

23. The polypeptide epitope according to claim 22, wherein the polypeptide epitope is a CTL-inducing peptide epitope.

24. The polypeptide epitope according to claim 22, wherein the polypeptide epitope is a HTL-inducing peptide epitope.

25. The method for eliciting an immune response in an individual comprising the administration of a composition comprising polypeptides according to claim 22, 23, or 24 to an individual in amounts sufficient to induce an immune response in the individual.

26. A composition comprising a pharmaceutically acceptable carrier and a polypeptide according to claim 22, 23, or 24.

27. The composition according to claim 26, wherein said carrier is an adjuvant.

28. A method of detecting a *P. falciparum* antigen comprising contacting a biological sample obtained from an individual with a polypeptide according to the claim 22, 23, or 24 and detecting the formation of an antibody-antigen complex or detecting the stimulation of T-cells obtained from the individual.

29. An isolated antibody, or fragment thereof, that specifically binds to a polypeptide as set forth in claim 22, 23, or 24.

SEQUENCE LISTING

<110> Epimmune, Inc.
The United States of America as Represented by the Secretary of the Navy
Sette, Alessandro
Doolan, Denise L.
Carucci, Daniel J.
Sidney, John
Southwood, Scott

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130 135 140

Cys Asn Ser Asn Phe His Ile Ile Phe Phe Asn Val Phe Asn Ile Phe
145 150 155 160

Phe Glu Lys Lys Lys Asn Lys Leu Phe Gln Asn Tyr Asn Leu Leu Arg
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Asn Ala Phe Ile Ile His Cys Lys Lys Asn Leu Ile Pro Tyr Phe Ile
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Phe Asn Asn Trp Tyr Asn Asp Glu Asn Tyr Asn Ile Tyr Leu Ile Lys
195 200 205

Tyr Lys Pro Leu Phe Met Phe Val Glu Asp Ser Ser Ser Phe Leu Tyr
210 215 220

Ala Phe Asn Lys Tyr Tyr Val Ser Asn Val Asn Thr Asp Asn Lys Glu
225 230 235 240

Asn Asn Val Asn Ile Asn Gln Glu Lys Lys Asn Ile Phe Val Asp Asn
245 250 255

Asp Lys Asn Ile Asn Gly Asp His Tyr Asp Asp Asp Val Glu Asn Ile
260 265 270

Glu Lys Lys Lys Asn Tyr Lys Glu Tyr Ile Tyr Lys Lys Asn Ile Tyr
275 280 285

Asp Ser Tyr Asn Asn Asp Ile Arg Glu Met Ser Leu Cys Phe Tyr Phe
290 295 300

Leu Leu Leu Asn Asn Ile Leu Arg Asp Ile Lys Cys Val Phe Phe Phe
305 310 315 320

Asn Leu Glu Ser Glu Lys Asn Thr Ile Asn Ala Phe Ser Ile Asn Tyr

325 330 335

Thr Gly Val Asn Phe Glu Ala Met Lys Gln Leu Asn Asp Lys Ala Ser
340 345 350

Leu Leu Phe Asp Asn Val Tyr Tyr Glu Lys Lys Glu Asn Ser Asn Arg
355 360 365

Glu Glu Ile Asn Asp Lys Val Ser Lys Gln Gly Cys Asn Leu Asn Asp
370 375 380

Ser Asp Ser Ser Asn Val Leu Tyr Ile Asn Ile Gln Asn Ile Lys Asp
385 390 395 400

Tyr Asp Ile Leu Tyr Lys Glu Asp Asn Lys Asn Tyr Asn Asp Val Glu
405 410 415

Asn Gln Met Leu Asn Arg Phe Met Asn Asn Val Lys Glu Glu Asn Val
420 425 430

Asp Leu Lys Asn Met Ala Leu His Ile Phe Phe Tyr Lys Ile Ile Asp
435 440 445

Glu Thr Glu His Val Val His Met Asn Lys Lys Glu Tyr Lys Tyr Phe
450 455 460

His Leu Val Met Lys Ile Leu Phe Leu His Asn Tyr Leu Leu Glu Lys
465 470 475 480

Met Asn Met Leu Asn Leu Cys Ile Asp Asn Leu Asn Glu Phe Asn Asp
485 490 495

Ile Tyr Lys Ile Ile Lys Glu Ala Val His Thr His Ile Cys Asp Tyr
500 505 510

Leu Asp Val Tyr Asn Phe Leu Leu Lys Leu Leu Gln Arg Tyr Glu Tyr
515 520 525

Ser Asn Ile Leu Lys Ser Ile Arg Asn Ser Asp Leu Leu Asn Phe Phe
530 535 540

Asn Ser Ser Ile Ile Gln Asn Leu Ile Asn Phe Leu Cys Gln Lys Ile
545 550 555 560

Ser Gln Asp Val Phe Ile Ile Glu Tyr Asp Asp Met Pro Phe Glu Asp
565 570 575

Lys Asp Asn Phe Glu Met Ser Tyr Lys Asn Ile Leu Lys Glu Lys Tyr
580 585 590

Glu Cys Leu Phe Pro Ile Asp Leu Ser Phe Leu Arg Asp Asp Ile Asn
595 600 605

Met Leu Cys Lys Arg Gly Asp Ala Thr Asn Asp Asp Asn Glu Asp Asn
610 615 620

Ile Ile Asn Ser Asn Asp Asp Arg Leu Glu Val Val Ser Lys Lys Lys
625 630 635 640

Glu Val Asn Asp Asp Asn Lys Asn Ile Val Thr Ile Asn Leu Ile Arg
645 650 655

Ile Lys Asn Glu Leu Val Glu Thr Phe Phe Tyr Leu Asn Asp Ile Ser
660 665 670

His Asn Asn Asn Asn Asn Asn Asn Cys Glu Val Asp Asn Met Ile Glu
675 680 685

Glu Lys Lys Arg Glu Met Val Leu Lys Ile Ile Phe Ile Asn Lys Cys
690 695 700

Leu Glu Tyr Asp Asn Asn Phe Phe Glu Leu Thr Gly Met Leu His Ile
705 710 715 720

Ser Glu Arg Glu Asn Val Val Asp Ile Phe Asn Ser Tyr Met Lys Leu
725 730 735

Ser Ser Leu Ser Arg Asn Leu Pro Phe Ala Asn Gln Lys Asp Asp Lys
740 745 750

Tyr Lys Leu Arg Arg Gln Gln Lys Asp Glu Arg Arg Lys Ala Ile Ile
755 760 765

Ala Lys Tyr Phe Tyr Ile Ser Ser Leu His His Pro Ile Val Ile Ser
770 775 780

Glu Asn His Pro Trp Ile Lys Tyr Tyr Ser Tyr Asn Ile Glu Lys Leu
785 790 795 800

Tyr Asp Tyr Leu Arg Asn Glu Glu Lys Lys Lys Gly Ile Thr Gln Arg
805 810 815

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Met Lys Val Leu Phe Asp Ser Ser Ser Glu Arg Glu Asp Asp Glu Lys
            820                 825                 830

Asp Gly Asp His Glu Ile Val Lys Ile Ser Asn Ile Ser Ser Asp Leu
        835                 840                 845

Lys Asn Lys Asn Lys Lys Asn Lys Arg Leu Ser Asp Ser Lys His Thr
    850                 855                 860

Asn Glu Lys Thr Ile Met Lys Lys Lys Leu Cys Thr Asn Ile Lys Leu
865                 870                 875                 880

Lys Lys Asn Asn Asp Ile Phe Glu Ile Leu Asp Asp His Phe Asp Glu
                885                 890                 895

Asp Ser Asp Arg Pro Glu Asp Met Asn Ser Ile Asn Glu His Gly Asn
            900                 905                 910

Lys Lys Glu Asp Ser Ser Asn Lys Lys Gly Lys Asn Glu Thr Lys Val
        915                 920                 925

Gly Lys Lys Gly Ser Lys Asn Ser Asn Ala Thr Thr Leu Ser Arg Lys
    930                 935                 940

Asp Glu Ile Leu Lys Lys Lys Glu Leu Ser Asn Glu Lys Lys Thr Tyr
945                 950                 955                 960

Glu Val Asp Leu Glu Arg Tyr Asn Asn Leu Glu Gln Lys Ile Val Lys
                965                 970                 975

Leu Ala Ser Asp Asp Ser Tyr Ala Glu Met Asn Val Trp Ser Leu Asp
            980                 985                 990

Ile Ile Ser Gly Tyr Asn Arg Leu  Val Asp Val Tyr Asn  Phe Asn Asn
        995                 1000                1005

Ile Thr  Asn Leu Ile Lys Ser  Val Asp Leu Gln Ile  Lys Ile Ser
    1010                1015                1020

Met Lys  Val Leu Asn Ser Met  Phe His Ile Ile Met  Tyr Thr Lys
    1025                1030                1035

Leu Lys  Asn Ile Lys Thr Gly  Lys Gln Lys Ser Asp  Ala Ile Arg
    1040                1045                1050
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Ser Ile Ile Leu Ile Tyr Arg Leu Thr Asn Asp Ile Phe Asn Lys
1055 1060 1065

Phe Lys Glu His Leu Ser Glu Lys Asp Val Val Gln Ile Gln Thr
1070 1075 1080

Val Leu Leu Ser Leu Gly Phe Gln Asn Ser Ser Tyr Asn Leu Phe
1085 1090 1095

Glu Glu Tyr Val Lys Leu Lys Lys Asp Thr Tyr Asn Ala Ser Ser
1100 1105 1110

Asn Asp Gly Lys Asp Glu Ala Gly Asn Lys Val Asp Glu Cys Val
1115 1120 1125

Ser Ser Gly Lys Lys Gly Lys Glu Asn Lys Lys Glu Glu Ser Asn
1130 1135 1140

Ser Lys Lys Lys Ile Ser Lys Gly Lys Lys Glu Asn Asn Asp Thr
1145 1150 1155

Lys Asp Val Asn Leu Lys Lys Ala Ser Lys Lys Gly Asp Val Asn
1160 1165 1170

Asn Ser Asn Ser Ile Ile Lys Ser Leu Asp Asp Ile Tyr Lys Tyr
1175 1180 1185

Lys Leu Glu Ser Val Lys Thr Tyr Ser Glu Leu Lys Ile Asp Glu
1190 1195 1200

Asn Lys Glu His Glu Phe Gln Leu Tyr Tyr Met Tyr Tyr Leu Leu
1205 1210 1215

Asp Arg Thr Thr Gly Asn Ile Lys Asp Ser Arg Val Leu Phe Thr
1220 1225 1230

Leu Asp Thr Trp Gln Tyr Asn Ile Leu Asn Leu Val Asp Arg Arg
1235 1240 1245

Lys Ser Ile Leu Val Ser Cys Pro Thr Ser Ser Gly Lys Thr Phe
1250 1255 1260

Ile Cys Tyr Tyr Val Met Asp Lys Val Leu Arg Leu Asn Asn Asp
1265 1270 1275

Ser Val Val Ile Tyr Val Ala Pro Asn Asp Thr Leu Ala Leu Gln
1280 1285 1290

Ile Tyr His Glu Val Asn Gly Arg Phe Ser Thr Lys Gly Tyr Ser
1295 1300 1305

Lys Tyr Gly Gly Asn Lys Leu Cys Ser Tyr Met Thr Asp Lys Tyr
1310 1315 1320

Ala Glu Glu Lys Ala Leu Asp Ser Gln Ile Ile Ile Ile Leu Pro
1325 1330 1335

Ser Ile Leu Glu Asn Ile Leu Leu Ser Tyr Tyr Ala Leu Asn Asp
1340 1345 1350

Met Asn Glu Asn Met Asn Val Ser Lys Phe Ile Ser Lys Ile Glu
1355 1360 1365

Tyr Ile Ile Phe Asp Glu Ile His Cys Ile Gly Asp Lys Glu Phe
1370 1375 1380

Tyr Gly Ser Gln Ile Glu Asn Ile Ile His Leu Ile Asn Cys Pro
1385 1390 1395

Phe Leu Ala Leu Ser Ala Thr Ile Gly Asn Ile Asn Cys Phe Tyr
1400 1405 1410

Ser Trp Leu Gln Asn Val Leu Leu Lys Lys Gly Arg Ser Ile Asn
1415 1420 1425

Asp Leu His Leu Ile Lys Phe Tyr Glu Arg Phe Ser Asp Leu Ile
1430 1435 1440

Leu Tyr Val Tyr Thr Asn Lys Asn Leu His His Leu Asn Pro Leu
1445 1450 1455

Thr Cys Phe Asn Phe Arg Asp Ile Leu Tyr Lys Gly Ile Asn Lys
1460 1465 1470

Asp Phe Tyr Cys Asn Pro Arg Glu Ile Tyr Glu Ile Ile Ile Ile
1475 1480 1485

Leu Phe Glu Leu Ala Arg Lys Lys Asn Phe Tyr His Leu Val Glu
1490 1495 1500

Phe Leu Glu Pro Ser Phe Tyr Phe Gln Tyr Thr Arg Cys Ile Asn

1505 1510 1515

Lys Lys Lys Phe Ile Tyr Tyr Met His Ser Val Lys Glu Met Ile
1520 1525 1530

Val Tyr Leu Ile Gln Asn Asn Tyr Ile Asn Asn Leu Glu Tyr Asp
1535 1540 1545

Met Ile Ile His Ile Leu Leu Ser Asn Tyr Met Lys Asn Ser Phe
1550 1555 1560

Tyr Ile Lys Asp Glu Asn Glu Glu Asp Ile Glu Arg Lys Asn Lys
1565 1570 1575

Ile Asn Asp Asn Asn Asn Asn Asn Ile Asn Cys Asp Asn Thr Lys
1580 1585 1590

Asn Asn Val Asp Asp Glu Asp Val Lys Thr Asn Asp Lys Val Ile
1595 1600 1605

Lys Lys Ser Asp Lys Val Val Val Lys Asn Leu Tyr Lys Ser Thr
1610 1615 1620

Ile Arg Asp Asn Val Pro Lys Glu Lys Leu Phe Gln Glu Leu Tyr
1625 1630 1635

Lys Arg Val Asn Phe Asp Glu Lys Tyr Ile Ser Asn Arg Thr Asn
1640 1645 1650

Asp Leu Val Lys Tyr Thr Glu Met Val Asn Met Glu Gln Glu Tyr
1655 1660 1665

Leu Asp Ser Asp Lys Leu Ile Glu Leu Leu Lys Lys Leu Glu Asp
1670 1675 1680

Ile Asn Phe Leu Pro Cys Ile Val Phe Asn Phe Glu Arg Lys Glu
1685 1690 1695

Leu Glu Asp Met Thr Ile Asn Leu Ile Asn Glu Leu Met Lys Arg
1700 1705 1710

Gln His Asp Lys Tyr Tyr Gly Asp Glu Glu Arg Ala Phe Asn Thr
1715 1720 1725

Lys Met Glu Asn Lys Met Arg Arg Glu Lys Tyr Glu Asn Met Leu
1730 1735 1740

Lys Gln Arg Glu Met Leu Leu Lys Met Lys Ser Met Ser Arg Asn
1745 1750 1755

Gln Arg Leu Glu Gln Asn Ile Asp Lys Glu Tyr Leu Asp Met Leu
1760 1765 1770

Ile Asp Asp Glu Ile Pro Glu Pro Pro Leu Asp Val Ser Glu Glu
1775 1780 1785

Tyr Asp Lys Asp Phe Tyr Phe Cys Asn Gln Lys Val Tyr Cys Asn
1790 1795 1800

Tyr Val Thr Glu Ile Glu Asp Leu Ile Lys Asp Ala Gln Lys Ala
1805 1810 1815

Ile Glu Gly Arg Lys Tyr Lys Ser Ile Leu Ile Glu Gly Leu Arg
1820 1825 1830

Arg Gly Ile Gly Leu His Tyr Glu Val Leu Pro Tyr Lys Phe Thr
1835 1840 1845

Ile Ile Val Glu Ser Leu Phe Arg Leu Gly Phe Val Lys Ile Ile
1850 1855 1860

Phe Ser Asn Lys Asn Leu Ser Leu Gly Ile Asn Ile Pro Cys Arg
1865 1870 1875

Ser Ile Ile Phe Ala Gly His Thr Ile Glu Leu Asn Ser Leu Met
1880 1885 1890

Phe Lys Gln Thr Ser Gly Arg Ala Gly Arg Arg Gly Phe Asp Leu
1895 1900 1905

Tyr Gly Asn Ile Ile Ile Trp Asn Ile Asn Phe Lys Asn Leu Lys
1910 1915 1920

Arg Leu Ile Thr Ser Pro Leu Gln Thr Leu Ser Gly Thr Tyr Ser
1925 1930 1935

Val Asn Phe Thr Asn Ile Cys Arg Ser Met Leu Leu Tyr Asn Ser
1940 1945 1950

Leu Lys Arg Ile Arg Glu Asn Glu Glu Gly Ser Leu Lys Asn Lys
1955 1960 1965

Val Ile Val Asn Lys Pro Asn Lys Lys Lys Lys Lys Asp Glu Thr
1970 1975 1980

Leu Ser Val Ala Glu Lys Glu Glu Ile Phe Glu Lys Asn Arg Ala
1985 1990 1995

Ile Asn Val Asn Tyr Phe Ser Arg Ile Asn Gly Ile Leu Ser Leu
2000 2005 2010

Phe Phe Asn Ser Leu Tyr Tyr Ile Asn Ser Phe Gln Glu Ser Glu
2015 2020 2025

Gln Asn Tyr Asn Asn Met Asn Asn Val Val Val Ser Gly Asp Asn
2030 2035 2040

Val Cys Ser Leu Thr Thr Asn Cys Gln Asn Gly Asn Glu Asn Gly
2045 2050 2055

Lys Gly His Ile Asn Asn Ile Ser Thr Cys Thr Thr Thr Ser Thr
2060 2065 2070

Ser Ser Val Asn Asn Met Glu Asn Asn Asn Asn Ser Asn Met Asn
2075 2080 2085

Gly Cys Gly Asp Lys Lys Ser Glu Gly Ser Glu Arg His Glu Met
2090 2095 2100

Ile Gln His Ile Leu His Glu Phe Asn Glu Tyr Lys Glu Asn Asp
2105 2110 2115

Lys Leu Ser Lys Phe Ile Asn Arg Glu Tyr Glu Tyr Asn Glu Leu
2120 2125 2130

Leu Val Glu Leu Leu Thr Asn Arg Lys Met Lys Asn Asn Lys Leu
2135 2140 2145

Gln Glu Glu Lys Glu Ile Asn Glu Leu Cys Phe Met Thr Arg Ala
2150 2155 2160

His Phe His Ile Phe Leu Asn Val Leu Ile Glu Met Glu Ala Leu
2165 2170 2175

Asp Glu Glu Gly Asn Ile Ile Asn Leu Thr Glu Leu Ser Ile Phe
2180 2185 2190

Leu Lys Lys Glu Tyr Asp Asn Asn Leu Ile Ile Thr Tyr Leu Leu
2195 2200 2205

Ile Lys Lys Val Leu His Asn Ile Ile Gly Asp Asn Thr Phe Leu
2210 2215 2220

Ser Ser Ser Val Val Ile Ser Leu Asn Arg Ile Ile Asp Ser Ile
2225 2230 2235

Thr Phe Glu Lys Asn Tyr Tyr Arg Ser Ile Ile Val Asp Asp Ser
2240 2245 2250

Thr Arg Gly Gln Phe Ile Leu Leu Phe Ile Leu Ser His Phe Ile
2255 2260 2265

Asn Lys Arg Lys Glu Asn Lys Ile Ala Leu Thr Lys Ala Leu Ile
2270 2275 2280

Asn Ser Gln Tyr Glu Glu Asn Lys Ser Lys Leu Glu Leu Phe Ser
2285 2290 2295

Ser Tyr Tyr Phe Pro Leu Leu His Ala Leu Pro Thr Ser Ile Gln
2300 2305 2310

Lys His Ile Asp His Ile Glu Asn Ile Leu Leu Lys Tyr Leu Val
2315 2320 2325

Asn Tyr Cys Leu Val Val Leu Ile Lys Leu Asn Leu Leu Asn Lys
2330 2335 2340

Lys Lys Ala Asn Leu Leu Pro Tyr Thr Lys Leu Tyr Ile Phe Glu
2345 2350 2355

Gln His Pro Cys Val Ser Leu Lys Asp Ile Phe Pro Lys Lys Glu
2360 2365 2370

Asn Ala Asp Tyr Phe Lys Phe Tyr Lys Ser Lys Val Ile Ile Ile
2375 2380 2385

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Val Leu Asn Glu Leu Asn Tyr Asp Asn Ala Gly Thr Asn Leu Tyr Asn
35 40 45

Glu Leu Glu Met Asn Tyr Tyr Gly Lys Gln Glu Asn Trp Tyr Ser Leu
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Lys Lys Asn Ser Arg Ser Leu Gly Glu Asn Asp Asp Gly Asn Asn Glu
65 70 75 80

Asp Asn Glu Lys Leu Arg Lys Pro Lys His Lys Lys Leu Lys Gln Pro
85 90 95

Ala Asp Gly Asn Pro Asp Pro Asn Ala Asn Pro Asn Val Asp Pro Asn
100 105 110

Ala Asn Pro Asn Val Asp Pro Asn Ala Asn Pro Asn Val Asp Pro Asn
115 120 125

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
130 135 140

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
145 150 155 160

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
165 170 175

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
180 185 190

Ala Asn Pro Asn Val Asp Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
195 200 205

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
210 215 220

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Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
225                 230                 235                 240

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
                245                 250                 255

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
            260                 265                 270

Lys Asn Asn Gln Gly Asn Gly Gln Gly His Asn Met Pro Asn Asp Pro
        275                 280                 285

Asn Arg Asn Val Asp Glu Asn Ala Asn Ala Asn Ser Ala Val Lys Asn
    290                 295                 300

Asn Asn Asn Glu Glu Pro Ser Asp Lys His Ile Lys Glu Tyr Leu Asn
305                 310                 315                 320

Lys Ile Gln Asn Ser Leu Ser Thr Glu Trp Ser Pro Cys Ser Val Thr
                325                 330                 335

Cys Gly Asn Gly Ile Gln Val Arg Ile Lys Pro Gly Ser Ala Asn Lys
            340                 345                 350

Pro Lys Asp Glu Leu Asp Tyr Ala Asn Asp Ile Glu Lys Lys Ile Cys
        355                 360                 365

Lys Met Glu Lys Cys Ser Ser Val Phe Asn Val Val Asn Ser Ser Ile
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Gly Leu Ile Met Val Leu Ser Phe Leu Phe Leu Asn
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Lys Asn Tyr Met Lys Ile Met Asn His Leu Met Thr Leu Tyr Gln Ile
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Gln Val Met Lys Arg Asn Gln Lys Gln Lys Gln Val Gln Met Met Ile
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Met Ile Lys Phe Met Gly Val Ile Tyr Ile Met Ile Ile Ser Lys Lys
65 70 75 80

Met Met Arg Lys Xaa Lys Lys Lys Lys Lys Lys Ser Thr Arg Thr Gln
85 90 95

Ala Lys Ser Leu Asp Thr Lys Leu Ile Asp Lys Asp Leu Met Asn Thr
100 105 110

Lys Gln Ile Glu Lys Glu Leu Leu Asp Thr Xaa Leu Ile Glu Asn Glu
115 120 125

Phe Ile His Asn Lys Leu Phe Asp Thr Asp Met Ile Glu Lys Glu Leu
130 135 140

Met Asp Thr Glu Leu Ile Glu Asn Glu Leu Met Asn Tyr Glu Leu Phe
145 150 155 160

Asp Lys Asp Thr Phe Phe Lys Glu Asn Tyr Phe Asn Asp Glu Gln Gln
165 170 175

Arg Thr Asp Glu Ser Asn Val Asp Gln Gln Asn Asp Met Tyr Val Ile
180 185 190

Lys Asn Asn Lys Asp Ser Met Lys Gly Asp Tyr Tyr Ile Lys Lys Lys
195 200 205

Lys Lys Lys Leu Val Thr Asp Asn Thr Lys Asp Leu Asn Lys Cys Ser
210 215 220

Ser Tyr Lys Ser Ser Lys Arg Asp Lys Phe Phe Glu Asn Ile Lys Arg
225 230 235 240

Glu Asn His Met Asp Asp Gln His Asn Glu Asn Ile Tyr Ile Asn Ile
245 250 255

Lys Asn Asn Lys Ser Thr His Thr Tyr Lys Lys Lys Asn Asn His Ile
260 265 270

Phe His Lys Asn Val Tyr Tyr Asn Ile Leu Ile Val Leu Tyr Tyr Leu
275 280 285

Phe Asn Gln His Ile Lys Lys Glu Leu Tyr His Phe Asn Met Leu Lys
290 295 300

Asn Lys Met Gln Ser Ser Phe Phe Met Asn Arg Phe Tyr Ile Thr Thr
305 310 315 320

Arg Tyr Lys Tyr Leu Asn Lys Lys Tyr Ile Asn Phe Ile Asn Phe Ile
325 330 335

Lys Val Leu Lys Glu Asn His Glu Gln Lys Leu Ser Glu Tyr Tyr Asp
340 345 350

Xaa Asp Ile Tyr Gln Lys Leu Tyr Ile Lys Gln Glu Glu Gln Lys Lys
355 360 365

Tyr Ile Tyr Asn Leu Ile Met Asn Thr Gln Asn Lys Tyr Glu Ala Leu
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Ile Lys Leu Leu Pro Phe Ser Lys Arg Ile Arg Lys Lys Ser Ile Phe
385 390 395 400

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Arg Asn Ile Ile Arg Ser Ala Lys Trp Asn Asn Lys Asn Ser Lys Ile
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Glu Leu Ser Lys Lys Arg Asp Ser Ser Asn Lys Tyr Lys Ser Ile Leu
        35                  40                  45

Lys Tyr Tyr Lys Asn Glu Asn Lys Thr Asn Lys Phe Ile Asp Lys Arg
    50                  55                  60

Lys Lys Asn Lys Trp Phe His Lys Asn Arg Lys Leu Gln Lys Lys Asn
65                  70                  75                  80

Ile Phe Asn Leu Asn Asp Asp Val Leu Phe Lys Glu Arg His Ile Ser
                85                  90                  95

Thr Asn Asp Phe Ile His Ser Asp Asn Ser Leu Lys Glu Thr Asp Gln
            100                 105                 110

Glu Asn Leu Asn Asp Asn Lys Lys Lys Gly Asn Lys Lys Tyr Asn Ala
        115                 120                 125

Met Leu Asp Lys Ile Glu Glu Lys Lys Leu Trp Lys Leu Lys Lys Tyr
    130                 135                 140

Glu Ile Lys Glu Lys Leu Arg Lys Phe Asp Glu His Phe Asp Glu Ile
145                 150                 155                 160

Gln Lys Asn Val Leu Gly Leu Asn Gly Thr Lys Gly Gly Ala Lys His
                165                 170                 175

Ser Met Val Ile Glu Asn Asn Lys Asn Lys Leu Asn Lys Val Ile His
            180                 185                 190

Glu Ser Lys Lys Arg Gln Asn Phe Glu Ile His Ala Ser His Lys Gly
        195                 200                 205

Ile Gly Ala Glu Lys Gly Lys Gln Asn Cys Tyr Asp Asp Gly Asp Asp
    210                 215                 220

Glu His Phe Asp Asp Asp Asp Asp Glu Gln Leu Asp Asp Gly Asp Asp
225                 230                 235                 240

Glu Gln Leu Asp Asp Asp Asp Asp Glu Gln Leu Asp Asp Asp Asp Asp
                245                 250                 255

Glu Gln Leu Asp Asp Asp Asp Asp Glu Gln Leu Asp Asp Asp Asp Asp
            260                 265                 270

Glu Gln Leu Asp Asp Ser Asp Asp Glu Ile Tyr Asp Asn Gln Lys Glu
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275 280 285

Tyr Ser His Asp Asp Glu Met Tyr Asn Asp Glu Lys Asn Val Asp Lys
290 295 300

Ala Asn Tyr Pro Lys Thr Thr Ser Asp Ser Gln Asn Glu Leu Thr Asn
305 310 315 320

Tyr Asn Ser Tyr His Thr Asp Asn Ser Asp Asn Glu Glu Ile Thr Lys
325 330 335

Leu Phe Asn Lys Glu Thr Leu Arg Ser Lys Lys Lys Gly Ser Asn Glu
340 345 350

Asn Ile Ser Lys Glu Lys Leu Asn Glu Leu Leu Glu Lys Tyr Lys Ile
355 360 365

Gly Asp Asn Ile Asn Ile Cys Asn His Phe Ile Asn Asn Thr Glu Glu
370 375 380

Glu Lys Gln Asn Ile Pro Ile Tyr Ile Tyr Ile Lys Asn Lys Glu Tyr
385 390 395 400

Asp Ile Lys Asp Val Ile Leu Leu Leu Asp Asp Tyr His Phe Glu Thr
405 410 415

Gln Gln Lys Ile Leu Tyr Arg Ile Tyr Tyr Ile Asn Met Phe Asn Lys
420 425 430

Lys Gly Thr Lys Ser Ile Tyr His Phe Ser Phe Phe Phe Ser Leu Ile
435 440 445

Asp Tyr Phe Ile Leu Asn Ile Tyr Lys Cys Leu Lys Tyr Asn Ile Lys
450 455 460

Val Cys Glu Leu Leu Gly Tyr Tyr Lys Asp Ile Ile Val Lys Tyr Cys
465 470 475 480

His Glu Met Lys Ala Glu Phe Tyr Leu Tyr Ile Ser Phe Leu Leu Leu
485 490 495

Ile Val Phe Ser Lys Ile Gln Arg Lys Ile Lys Thr Asn Ile Phe Phe
500 505 510

Lys Lys Lys Lys Lys Ile Leu Gln Asp Tyr Val Ile Leu Asn Glu Asp
515 520 525

Asn Ala Asn Arg Lys Ile Asp Val Tyr Ile Tyr Arg Arg Ile Leu Lys
530 535 540

Ser Val Asp Met Phe Ser Ser Ile Phe Glu Asn Tyr Asn Asn Glu Asn
545 550 555 560

Ile Tyr Ile Ser Asn Ile His Phe Ala Val Leu Phe Leu Thr Leu Thr
565 570 575

Val Tyr Pro Ile Asn Asn Phe Ile Asp Asp Asn Asn Met Ser Asn Val
580 585 590

Val Glu Asn Lys Ile Leu Asn Pro Gln Lys Asn Leu Ile Ile Asn Asn
595 600 605

Asn Pro Phe Leu Asp Ile Asn Lys Asn Asn Ile Asn Asp Glu Lys Leu
610 615 620

Leu Tyr Lys Met Asn Tyr Leu Lys Gln Asp Ile Asn Asn Ile Asn Asn
625 630 635 640

Tyr Asn Gln Gln Lys His Pro Ile Ile Ser Phe Ile Ile Glu Ile Leu
645 650 655

Glu Leu Leu Phe Tyr Asn His Phe Tyr Thr Asn Asn Ala Asn Leu Leu
660 665 670

Asn Leu Lys Asp Tyr Gln Lys Tyr Asp Trp Val Phe Asn Met Asn Thr
675 680 685

Tyr Glu Asn Tyr His Asn Ile Glu Ala Cys Leu Lys Lys Leu Glu Val
690 695 700

Tyr Tyr Ser Phe Ser Ser Phe Glu Asp Val Ile Cys Glu Asn Asn Lys
705 710 715 720

Gly Gly Lys Glu Phe Glu His Asn Glu Ile Asn Asn Glu Ile Val Asn
725 730 735

Asp Leu Gly Ile Phe Tyr Arg Lys Lys Glu Phe Lys Asn Ser Leu Ile
740 745 750

Leu Leu Asn Leu Tyr Asn Ile Ile Met Glu Asn Thr Leu Glu Tyr Asn
755 760 765

Pro Ser Phe Phe Tyr Leu Ser Phe Lys Ile Leu Asn Thr Leu Leu Tyr
770 775 780

Asn His Ile Thr Ser Ile Lys Glu Gly Ile Leu Asp Lys Asn Lys Ile
785 790 795 800

Pro His Val Ser Glu Lys Glu Lys Gln Lys Ile Gln Thr Ile Asn Asn
805 810 815

Ser Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
820 825 830

Asn Ile Ser Asn Asn Met Tyr Asp Lys Phe Asp Leu Ser Phe Ile Ile
835 840 845

Phe Lys Asn Ile Phe Phe Phe Leu Lys Ile Tyr Ile Asp Asn Asp Ile
850 855 860

Asn Ile Tyr Ile Leu Ile Asn His Val Ile Ile Pro Ser Leu Phe Tyr
865 870 875 880

Leu Tyr Met Asn Phe Leu Lys Phe Ile Val Thr Asn His Ile Lys Leu
885 890 895

Asp Phe Ile Asn Ile Ile Asn Val Ala Lys Asn Ile Asn Ile Lys Glu
900 905 910

Gly Asn Asp Phe Leu Phe Glu Glu Asp Lys Thr Tyr Glu Leu Tyr Gln
915 920 925

Lys Tyr Leu Ile Ile Leu Leu Tyr Ile Phe Lys Leu Ile Glu Tyr Ser
930 935 940

Gln Asn His Asp Ile Lys Pro Ile Ile His Lys Thr Thr Thr Glu Gly
945 950 955 960

Asn Ile Ser Phe Phe Thr Pro Lys Tyr Ala Asn Asn Gln Asn Pro Lys
965 970 975

Asp Phe Ile Phe Met Gln Asn Asn Gln Thr Lys Leu Ala Glu Met Lys
980 985 990

Ser Ile Lys Lys Lys Met Lys Gln Gln Arg Lys Phe Asp Tyr Asn Glu
995 1000 1005

Val Ile Lys Ile Cys Thr His Ile Ser Tyr Tyr Lys Tyr Ile Tyr
1010 1015 1020

Ile Tyr Ile Tyr Ile Phe Ile Tyr Leu Phe Ile Tyr Ile Trp Leu
1025 1030 1035

His Leu Ile Ile Ile Phe Ile Phe Val Asp Glu Glu Gly Glu Gln
1040 1045 1050

Leu Tyr Leu Gly Ser Lys Ser Lys Arg
1055 1060

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Leu Ile Arg Pro Met Leu Val Lys Leu Arg Pro Lys Leu Val Lys Leu
20 25 30

Arg Pro Met Leu Val Lys Leu Gly Pro Ile Leu Val Lys Leu Arg Pro
35 40 45

Met Leu Val Lys Leu Arg Pro Met Leu Ala Lys Leu Arg Pro Met Leu
50 55 60

Ala Lys Leu Arg Pro Lys Leu Val Lys Leu Arg Pro Lys Leu Val Lys
65 70 75 80

Leu Arg Pro Ile Ser Val Asn Ala Lys Pro Gln Leu Val Asn Val Arg
85 90 95

Pro Val Leu Val Lys Ile Arg Pro
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Arg Lys Lys Arg Ser Phe Ala Lys Ser Lys Glu Asp Glu Arg Asn Lys
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Ser Glu Glu Asp Leu Ser Glu Asp Asp Lys Asn Lys Asp Tyr Ser Ser
35 40 45

Ala Ser Glu Ser Asn Phe Tyr Lys Tyr Lys Lys Arg Lys Asn Asn Thr
50 55 60

Tyr Glu Tyr Lys Asp Asp Lys Asp Tyr Thr Ser Tyr Asp Asn Lys Phe
65 70 75 80

Arg Lys Ile Arg Asn Ile Asp Asp Ile Leu Glu Met Lys Pro Asn Ile
85 90 95

Leu Leu Ser Arg Phe Ile Phe Ile Tyr Lys Leu Val Asp Asn Ile Ser
100 105 110

Glu Asp Glu Ile Asp Glu Leu Ile Arg Asn Ile Ser Ile Asn Asn Ala
115 120 125

Phe Ser Leu Pro Val Asn Ile Tyr Ile Asn Lys Leu Ser Phe Phe Ser
130 135 140

Ile Lys Asp Glu Leu Phe Val Lys Glu Asn Leu Glu Phe Leu Lys Asn
145 150 155 160

Asn Ser Tyr Phe Asn Ile Ile Gln Gln Lys Ile Gln Ser Asn Phe Leu
165 170 175

Leu Glu Asn Arg Ile Asn Asp Asp Gln Cys Cys Ile Ile Glu Phe Pro
180 185 190

Ser Asp Glu Ala Ser Gly Lys Leu Phe Ser Leu Tyr Glu Lys Asp Asn
195 200 205

Cys Ile Glu Ile Lys Asn Asn Ile Ser Tyr Ile Phe Pro Leu Phe Lys
210 215 220

Leu Lys Asn Lys Gly Lys Asn Val Glu Glu Lys Thr Gly Ser Asn Lys
225 230 235 240

Val Ser Asp Trp Tyr Cys Ser Ala Cys Asn Phe Leu Asn Phe Ser Arg
245 250 255

Arg Thr Ala Cys His Phe Cys Lys Ala Pro Lys Thr Ser Asp Ala Lys
260 265 270

Leu Val Asp Lys Glu Thr Ser Thr Ile Ser Thr Phe Ile Lys Asn Asn
275 280 285

Ile Asn His Gln Glu Asn Asn Leu Tyr Leu Ile Asn Asn Lys Asn Leu
290 295 300

Tyr Asn Asn Met His Val Asp Lys Gly Thr Tyr Asn His Met Leu Ser
305 310 315 320

Asp Pro Leu Asn Met Gln Lys Val Tyr Val Tyr Asn Asn Met Glu Asp
325 330 335

Asn Tyr Glu Asn Ile Leu Asn Asp Thr Tyr Lys Asp Ala Asn Asn Asn
340 345 350

Ile Ser Asn Asn Asn Asn Asn Asn Asn Asn Asn Asp Asn Asp Tyr Asn
355 360 365

Asn Asn Asn Asn Asn Asn Asn Asn Ser Lys Asn Asn Asn Tyr Asn Asn
370 375 380

Asn Tyr Asn Ser Asn Tyr Asn Arg Gly Asn Glu Asn Asn His Leu Lys
385 390 395 400

Leu Ser Asn Asn Asn Ile Phe Phe Ser Tyr Asn Pro Phe His Lys Phe
405 410 415

Asn Glu Asp Ser Gln Asn Tyr Glu Asn Ile Asn Lys Glu Ile Ile Cys
420 425 430

Asp Asp Gln Asn Thr Asn Met Leu Ile Leu Lys Asn Met Asp Gly Asn
435 440 445

Ile Leu Ile Lys Asp Phe Ile Gln Phe Leu Asn Val Thr Phe Asp Lys
450 455 460

Asn Asp Val Ser Cys Ile Tyr Leu Phe Asn Asp Ile Lys Gly Ser Ser
465 470 475 480

Lys Lys Lys Gly Phe Cys Phe Ile Glu Phe Tyr Asn Ile Asn Met Ala
485 490 495

Lys Lys Val Met Asn Asn Met Glu Lys Asn Tyr Tyr Leu Asn Phe Gln

500 505 510

Asp Asn Tyr Leu Lys Leu Asp Tyr Val Tyr Glu Lys Glu Lys Gln Tyr
515 520 525

Phe Phe Asn Cys Ile Gln Met Ala Lys Leu Asp Ile Ser Lys Ser Ser
530 535 540

Ala Thr Val Val Lys Asn Asn Ile Pro Tyr Phe Asn Phe Phe Val Asn
545 550 555 560

Tyr Phe Glu Ala Val Val His Met Asn Ile His Cys Tyr Thr Tyr Phe
565 570 575

Leu Met Trp Ser Ser Gln Ile Ile Ile Leu Lys Lys Gly Lys Pro Glu
580 585 590

Leu Ser Glu Phe Phe Phe Asp Tyr Asn Ser Gln Tyr Tyr Tyr His Pro
595 600 605

Leu Tyr Gln Leu Tyr Phe Asp Asn Asn Thr Lys Tyr Tyr Met Ser Leu
610 615 620

Ser Lys Gly Tyr Tyr Ile Trp Glu Asp Gly Leu Lys Cys Leu Leu Arg
625 630 635 640

Val Tyr Leu Asp Asn Leu Gly Glu Asn Val Tyr Glu Arg Glu Asn Tyr
645 650 655

Asp Lys Lys Phe Ser Leu Met Asp Ala Ser Lys Asn Lys Glu His Glu
660 665 670

Glu Thr His Gln Gln Ala Arg Ile Asn Asp Asp His Lys Tyr Asp Asn
675 680 685

Ile Ser Asn Asn Asn Ile Ile Asn Gly His Met Leu Glu Gln Lys Leu
690 695 700

Ser Asn Tyr Lys Ile Glu Lys Glu Asn Glu Lys Lys Asn Asn Asn Glu
705 710 715 720

Asn Val Ile Leu Asn Lys Ile Ser Ser Phe Val Glu Lys Ala Lys Glu
725 730 735

Ile Ala Leu Ala Ser Lys Lys Asn Ile Glu Gln Met Asn Met Asn Asp
740 745 750

Asn Asn Leu Ser Ile Leu Glu Lys Lys Asn Lys Glu Ile Ile Lys Lys
755 760 765

His Phe Thr Thr Asp Ser Ala Asp Asp Glu Asp Glu Glu Asn Asp Asn
770 775 780

Asp Asn Asp Asn Asp Glu His Asp Asp Asp His Asp Asn Glu Lys Glu
785 790 795 800

Asp Asn Asp Asp Glu Leu Asn Asn Val Ser Ile Lys Asn Lys Asp Asn
805 810 815

Ile Ser Asp Ile Asn Ile Ile Glu Lys Gln Ser Asn Asp Asp His Asn
820 825 830

Asn Lys Gln Arg Ile Asp Asn Ser Ser Tyr Tyr Asp Tyr Lys Lys Asn
835 840 845

Val Lys Leu Ser Asp Asn Ile Ser Asn Asn Ile Asn Asn Asn Ile Pro
850 855 860

Tyr Gln Asn Asn Asn Asn Asp Met Lys Lys Gly Tyr Thr Asn Val Ser
865 870 875 880

Asn Asn Ser Phe Asn Asn Ser Asn Ile Tyr Asn Asn Asn Asn Glu His
885 890 895

Ile Asn Asn Asn Asp Glu Lys Asp Val Ile Ser Glu Gln Ser Glu Lys
900 905 910

Asn Ile Asn Ile Cys Phe Ile Cys Leu Arg Lys Phe Leu Asn Glu Glu
915 920 925

Met Leu Gln Arg His Ile Asp Val Ser Asn Leu His Lys Lys Asn Val
930 935 940

Glu Ile Leu Ser Asp Pro Val Leu Ser Asn
945 950

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Met Lys Ile Arg Tyr Asp Lys Cys Ser Ser Thr Lys Asp Leu Asn Tyr
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Phe Phe His Leu Lys Leu Gly Phe Phe Val Cys Tyr Lys Asn His Asn
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Asp Lys Tyr Ser Phe Lys Asn Lys Ile Leu Gln Lys Asn Asp Thr Ile
35 40 45

Leu Phe Phe Lys Lys Lys Lys Lys Phe Met Tyr Leu Arg Lys Lys Lys
50 55 60

Lys Lys Lys Lys Lys Lys Ile Leu Ile Gln Ile Ile Gln Glu Tyr Asn
65 70 75 80

Lys Tyr Asn Glu Tyr Phe Lys Tyr Asn Ser Asn Leu Glu Gly Asn Gln
85 90 95

Gly Phe Asn Lys Lys Pro Glu Lys Asn Lys Asn Thr Lys Gly Asn Val
100 105 110

Tyr Thr Asp His Thr Asn Gln Asn Ala Lys Ser Lys Ile Tyr Asn Tyr
115 120 125

Asp Met Asn Asp Asp Ser Tyr Ser Asn Tyr Val Asn Asn Asn Asn Val
130 135 140

Phe Arg Ile Ser Ser Phe Leu Ile Leu Asn Asn Glu Phe Phe Gly Tyr
145 150 155 160

Pro Leu Gln Phe Val Cys Glu Thr Glu Gly Arg Ser Arg Asn His Glu
165 170 175

His Tyr Pro Asp Val His Gly Asp Asn Ile Lys Tyr Asn Lys Cys Asp
180 185 190

Asp Asn Lys Tyr Asn Lys Cys Asp Asp Asn Lys Tyr Asp Lys Cys Asp
195 200 205

Asp Asn Lys Tyr Asn Lys Cys Asp Asp Asn Lys Tyr Asp Thr Cys Asp
210 215 220

Asp Asn Lys Tyr Asp Thr Cys Asp Asp Asn Lys Tyr Asp Thr Cys Asp
225 230 235 240

Asp Asn Lys Tyr Asn Lys Tyr Asp Asp Asp Lys Tyr Asp Thr Cys Asp

245 250 255

Asp Asn Lys Tyr Asn Lys Tyr Asp Asp Asp Lys Tyr Asn Lys Tyr Asp
260 265 270

Asp Asp Lys Tyr Asn Lys Tyr Asp Asp Asp Lys Tyr Glu Lys Ser Arg
275 280 285

Lys Lys Lys Lys Leu Asn Asn Leu Tyr Lys Thr Ile Leu Thr Lys Lys
290 295 300

Lys Arg Lys Lys Met Asn Ser Asn Leu Cys Val Ile Asn Lys Ile Tyr
305 310 315 320

Lys Tyr Pro Ile Lys Tyr Cys Glu Leu Asn Ser Lys Ala Phe Val Phe
325 330 335

Phe Ile Ile Lys Asn Val Gly Val His Lys Ile Thr Tyr Tyr Ser Tyr
340 345 350

Asn Lys Leu Phe Ser Lys Asp Gly Val Leu Asn Gln Gly Ile Gln Ile
355 360 365

Cys Lys Leu Tyr His Val Asn Lys Asn Lys Lys Ile Lys Gln Ile Ile
370 375 380

Phe Glu Ala Leu Lys Asn Lys Ile Thr Phe Ser Tyr Asp Asn Asn Pro
385 390 395 400

Asn Asn Ile Lys Lys Lys Ile Tyr Lys Phe Leu Lys Lys Asn Cys Ala
405 410 415

Tyr His Asp Leu Ile Lys Leu Phe Tyr Phe Lys Gly His Lys Gln Arg
420 425 430

Glu Lys Cys Asn Lys Lys Leu Asn Met Glu Lys Thr Phe Gly Val His
435 440 445

Lys Ser Ser Arg Tyr Asn Tyr Lys Thr Tyr Lys Lys Lys Lys Lys Ile
450 455 460

Asp Met Cys Lys Asn Tyr Cys Asp Asp Ile Leu Asp Thr Tyr Asn Ser
465 470 475 480

Lys Tyr Tyr Lys Gly Glu Leu Ser Gly Gln His Lys His Ile Lys Met

485 490 495

Thr Gly Glu Gln Lys Glu Glu His His Ile Lys Tyr Thr His Leu Asn
500 505 510

Phe Asn His Gly Lys Asp Glu Thr Phe Tyr Lys Glu Leu Tyr Lys Cys
515 520 525

Asn Tyr Ile Glu Lys Tyr Ile Ser Ser Val Asn Tyr Phe Leu Leu Glu
530 535 540

Arg Arg Arg Met Phe Asn Lys Tyr Lys Gln Gln Glu Leu Cys Val Asn
545 550 555 560

Lys Asn Glu Glu Asn Asn Lys Asn Lys Asn Asp Asp Asp Asn Lys Asn
565 570 575

Asp Asp Asp Asn Lys Asn Asp Asp Asp Asn Asn Lys Asn Asp Asp Asp
580 585 590

Asn Lys Asn Asp Asp Asp Asp Asn Lys Asn Asp Asp Asp Asn Lys Asn
595 600 605

Asp Asp Asp Asp Asn Lys Asn Asp Asp Asp Asp Asn Asn Lys Asn Asn
610 615 620

Ile Gln Cys Asp Asn His Ser Asp Asn Ile Tyr Met Cys Gly Thr Tyr
625 630 635 640

Gly Asn Met Glu Asn Tyr Asn Val Pro His Ser Thr Asn Asn Thr Asn
645 650 655

Leu Gln Ser Ile Lys Lys Arg Ile Ile Asn Met Asn Ile Leu Asp Asn
660 665 670

Ile Arg Cys Asn Lys Thr Tyr Lys Tyr Ile Asp Lys Asn Lys Phe Lys
675 680 685

Cys Phe Thr Tyr Tyr Ser Cys Lys Asn Tyr Asn Val Cys Lys Lys Ile
690 695 700

Ile Glu Lys Tyr Lys Leu Tyr Lys Phe Leu Lys Lys Lys Lys Ile Glu
705 710 715 720

Gly Tyr Met Ile Leu Asn Phe Leu Asn Phe Asn Lys Glu Leu Ile Tyr
725 730 735

Tyr Asn Glu His Lys Lys Asp Met Ser Thr Leu His Asp Asn Leu Phe
740 745 750

Asp Val Ile Ser Asn Asn Gln Asn Glu Asn Val Lys Tyr Asn His Ile
755 760 765

Cys Asn Asn Asn Lys Tyr Asp Trp Phe Phe Asn Ser Phe Asp Tyr Val
770 775 780

Gly Asn Leu Glu Glu Ser Ile Thr Cys Phe Asn Asn His Lys Lys Lys
785 790 795 800

Glu Asn Met Lys Asn Ile Lys Asn Ile Lys Lys Lys Lys Lys Lys Asn
805 810 815

Leu Phe Tyr Asn Glu Gln His Asn Ile Lys Asn Asn Lys Asn Asp Tyr
820 825 830

His Phe Asp Lys Tyr Pro Ser Ser Leu Tyr Ser His Leu Thr Asn Lys
835 840 845

Lys Met Val Asn Asn Thr Glu Val Asn Asn Ile Lys Asp Glu Asn Ser
850 855 860

Leu Gln Met Tyr Ile Ile Asn Lys Asp Val Thr Lys Asn Lys Asp Gly
865 870 875 880

Asn Leu Leu Leu Asn Ser Tyr Tyr Asn Ser Lys Leu Gly Lys Ser Ile
885 890 895

Asn Thr Cys Ser Lys Glu Ile Tyr Lys Glu Glu His Lys Asn Val Tyr
900 905 910

Ile Tyr Asn Lys Lys Ile Thr Lys Met Asn Ile Lys Met Lys Thr Glu
915 920 925

Gln Lys Tyr Ile Cys Val Asp Ser Lys Arg Asn Thr Arg Thr Tyr Asn
930 935 940

Ser Lys Asn Ile Arg Thr Tyr Asn Ser Lys Asn Ile Arg Thr Tyr Asn
945 950 955 960

Ser Lys Asn Ile Arg Thr Tyr Asn Arg Lys Asn Ile Arg Thr Tyr Asn
965 970 975

Arg Lys Asn Ile Arg Thr Tyr Asn Arg Lys Asn Ile Arg Thr Tyr Asn
980 985 990

Arg Lys Asn Ile Arg Cys Asn Asn Arg Lys Lys Phe His Leu Asn Arg
995 1000 1005

Asn Lys Lys Lys Asn Gly Cys Val Lys Lys Tyr Lys Leu Tyr Asp
1010 1015 1020

Glu Arg Asn Thr Leu Val Tyr Lys Asn Lys Ile Gly Ser Asn His
1025 1030 1035

Phe Phe Leu Lys Glu Glu Ile Gly Lys Ser Thr Lys Lys Leu Asn
1040 1045 1050

Asp Ile Phe Glu His Ile Ser Asn Tyr Thr Asn Arg Ile Ser Lys
1055 1060 1065

Asn Ile Asn Ile Thr Asn Lys Asn Arg Tyr Asp Asp Tyr Pro Phe
1070 1075 1080

Asp Phe Leu Ser Lys Asp Lys Ile Glu Tyr Ile Ser Met Leu Ser
1085 1090 1095

Pro Thr Ile Asn Glu Ile Lys Thr Leu Asn Thr Ile Leu Thr Ile
1100 1105 1110

Pro Leu Ile Lys Met Asn Glu Tyr Glu Lys Asn Cys Ile Trp Arg
1115 1120 1125

Phe Arg Phe Gln Leu Leu Asn Arg Lys Glu Thr Leu Gly Lys Phe
1130 1135 1140

Leu Lys Ser Ile Asn Trp Asn Asn Lys Glu Glu Glu Glu Glu Ala
1145 1150 1155

Ile Ile Leu Leu Asn Lys Trp Ala Lys Pro Gly Ile Glu Asn Cys
1160 1165 1170

Ile Glu Leu Phe Tyr Ser His Leu His His Tyr Val Ile Lys Lys
1175 1180 1185

Tyr Ile Ile Asp Ile Ile Lys Asn Ser Lys Lys Glu Glu Ile Lys
1190 1195 1200

Leu Tyr Leu Phe Gln Leu Val Gln Ser Leu Arg Thr Phe Asn Tyr
1205 1210 1215

Gln His Ile Asp Asn Leu Phe Ile Asn Thr Leu Ile Gln Lys Cys
1220 1225 1230

Ile Lys Ser Lys Lys Leu Ser Ile Tyr Phe Tyr Trp Phe Leu Leu
1235 1240 1245

Ser Glu Ala Lys Asp Lys Ile Lys Gly Lys Leu Tyr Leu His Ile
1250 1255 1260

His Lys Leu Phe Ile Asn Lys Leu Met Thr Ser Asn Ile Arg Lys
1265 1270 1275

Asn Lys Ile Ile Leu Asp Ile Leu Lys Asn Gln Asn Arg Phe Arg
1280 1285 1290

Asn Gln Leu Leu Tyr Leu Thr Lys Ile Ala Lys Asn Lys Thr Asp
1295 1300 1305

Arg Ile Gln Asn Lys Thr Arg Lys Leu Arg Asn Phe Leu Phe Tyr
1310 1315 1320

Tyr Arg Thr Asn Tyr Gly Tyr Ile Asn Ile Lys Asp Phe Ile Lys
1325 1330 1335

Asn Asn Ile Phe Ile Ser Asp His Asn Val Tyr Asp Phe Leu Asp
1340 1345 1350

Ile Cys Lys Met Lys Arg Glu Asn Ser Leu Asp Thr Pro Met Arg
1355 1360 1365

Gly Asp Asn Ile Gly Gln Pro Ser Tyr Leu Gly Met Val Pro Gly
1370 1375 1380

Met Gly Lys Ser Thr Asp Asp Ser Lys Asn Val Tyr Gly Asp Asp
1385 1390 1395

Asn Lys Asn Val Tyr Gly Asp Asp Asn Lys Asn Val Tyr Gly Asp
1400 1405 1410

Asp Ser Lys Asn Ile Tyr Cys Asp Asp Asn Lys Asn Val Tyr Gly
1415 1420 1425

Asp Asp Asn Lys Asn Ile Tyr Gly Asp Asp Ser Lys Asn Ile Tyr
1430 1435 1440

Gly Asp Asp Asn Lys Asn Ile Phe Ser Asp Asp Asn Lys Asn Leu
1445 1450 1455

Tyr Ser Asp Asn Asn Asn Asn Lys His Ile Arg Tyr Asn Lys Tyr
1460 1465 1470

Val Lys Asn Ile Ser Tyr Glu His Phe Asn Glu Tyr Pro Tyr Asp
1475 1480 1485

Asn Lys Lys Ser Arg Asn Ile Tyr Thr Cys Asn Lys Asp Ile Cys
1490 1495 1500

Asn Ser Ile Tyr Tyr Leu Asp Asn Glu Leu Thr Ile Asn Tyr Asp
1505 1510 1515

Ile Lys Asp Asp Leu Tyr Phe Phe Gln Tyr Lys Arg Ser Ser Asp
1520 1525 1530

Glu Lys Leu Leu Asn Thr Asp Leu Ser Asn Asp Ser Asn Asp Met
1535 1540 1545

Ile His Tyr Ile Asp Asp Ser Lys Asn Val Lys Ile Glu Arg Asn
1550 1555 1560

Arg Asp Asn Ser Phe Phe Ser Asn Phe Leu Gln Phe Asn Asp Asn
1565 1570 1575

Leu Asp Phe Phe Leu Asn Ala Thr Tyr Ser Asp Glu Asp Asn Asn
1580 1585 1590

Tyr Glu Ile Leu Asp Asp Ser Ile Asn Phe Val Gln Lys Gln Lys
1595 1600 1605

Ile Lys Lys Ile Lys Thr Pro Leu Ile Leu Pro Ile Asp Pro Asn
1610 1615 1620

Ile Glu Leu Leu Ser Phe Leu Pro Glu Gln Ser Tyr Val Leu Arg
1625 1630 1635

Ser Ser Leu Tyr Pro Ile Val Ile Ala Cys Leu Val Arg Lys Lys
1640 1645 1650

Ile Lys Leu Tyr Asn Glu Asn Tyr Asn Asn Leu Ile Ile Asn Asn
1655 1660 1665

His Thr Phe Tyr Lys Asn Asp Gln Asn Lys Asp Asn Ile Ile Asn
1670 1675 1680

Asn Leu Ser Tyr Asp Lys Ser Tyr His Ser Tyr Tyr Asn Ser Gln
1685 1690 1695

Phe Ile Lys Thr Leu Gln Asn Ser Phe Glu Ser Thr Thr Ser Leu
1700 1705 1710

Asn Tyr His Tyr Asn Phe Leu Lys Cys Ser Asn Asn Asn Ile Phe
1715 1720 1725

Tyr Lys Asn Lys Lys Ile Glu Arg Ile Lys Pro Asn Thr Ser Ile
1730 1735 1740

Gln Lys Ala Phe Pro Ser Asn Glu Asn Ile Leu Asn Arg Asn Gln
1745 1750 1755

His Val Tyr Tyr Ser Asn Asn Gln Ile Val His Asn Ile Lys Lys
1760 1765 1770

Met Asn Lys His Lys Arg Asp Asp Tyr Met Ile Asn Glu Lys Val
1775 1780 1785

Leu Pro Cys Val Ser Asn Ser Cys Leu Gly Asp Lys Leu Met Pro
1790 1795 1800

Ser His Asp Lys Met Arg Ser Ser His Asp Lys Met Met Pro Ser
1805 1810 1815

His Asp Lys Met Met Pro Ser His Asp Lys Leu Met Ser Pro His
1820 1825 1830

Tyr Thr Leu Met Ser Ser His Asp Lys Pro Val Ala Pro Ser Gly
1835 1840 1845

Val Ser Ser Leu Gly Glu Lys Lys Ser Lys Asp Glu Lys Lys Asn
1850 1855 1860

Arg Lys Lys Tyr Asn Glu Ile Tyr Gln Leu Ser Ile Lys Lys Tyr
1865 1870 1875

Ile Tyr Lys Ala Gly Asp Asp Leu Arg Gln Asp His Leu Val Ile

1880 1885 1890

Gln Ile Ile Tyr Val Met Asp Asn Ile Trp Lys Arg Tyr Gly Leu
1895 1900 1905

Asp Leu Lys Met Thr Leu Tyr Arg Val Leu Ala Leu Ser Thr Asp
1910 1915 1920

Asp Gly Phe Ile Glu Phe Val Asp Tyr Ala Glu Ser Ile Ser Ser
1925 1930 1935

Ile Lys Lys Asn Tyr Lys Gly Glu Ile Arg Gln Tyr Phe Ile Asp
1940 1945 1950

Asn Ser Thr Cys Ser Ser Ser Pro Leu Gly Phe Asp Thr Glu Ile
1955 1960 1965

Leu Gln Asn Phe Ile Ser Ser Cys Ala Gly Tyr Ser Val Ile Thr
1970 1975 1980

Tyr Ile Leu Gly Ile Gly Asp Arg His Leu Asp Asn Leu Met Val
1985 1990 1995

Thr Lys Asp Gly Arg Phe Phe His Ile Asp Phe Gly Tyr Ile Phe
2000 2005 2010

Gly Glu Asp Pro Lys Pro Phe Ser Pro Pro Met Lys Leu Cys Lys
2015 2020 2025

Glu Met Ile Glu Ala Met Gly Gly Ala His Ser Ile Gly Tyr Glu
2030 2035 2040

Gln Phe Leu Lys Lys Cys Cys Leu Ala Tyr Lys Tyr Leu Arg Tyr
2045 2050 2055

His Ser Gln Leu Ile Ile Ser Leu Leu Asp Ala Met Cys Asp Ala
2060 2065 2070

Gly Leu Lys Asp Met Lys Met Ser Pro Glu Leu Cys Val Leu Lys
2075 2080 2085

Val Gln Glu Lys Phe Arg Leu Asp Leu Asn Asp Glu Ala Ala Glu
2090 2095 2100

Ile Tyr Phe Leu Ser Val Ile Asn Ala Ser Val Lys Thr Leu Phe
2105 2110 2115

Pro Val Val Val Asp Lys Leu His Glu Trp Ala Leu Asn Trp Lys
2120 2125 2130

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Phe Asp Asp Phe Lys Ile Asn Tyr Ser Tyr Lys Thr Lys Asn His Leu
35 40 45

His Glu Asn Asp Lys Ile Lys Glu Glu Asp Asp His Glu Ile Lys Arg
50 55 60

Lys Leu Ile Lys Leu Ile Asn Thr Asn Phe Tyr Ile Asp Lys Cys Ile
65 70 75 80

His Phe Lys Lys Phe Ser Lys Asp Glu Leu Tyr Lys Thr Phe Ile Tyr
85 90 95

Ser Asn Phe Leu Thr Lys Ala Leu Ile Leu Tyr Pro Ser Leu Met Pro
100 105 110

Tyr Val Glu Cys Ile Ile Glu Lys Ile Lys Lys Ile Lys Asn Glu Asn
115 120 125

Ile Thr Phe Phe Pro Ala Ile Glu Gln Phe Asn Phe Ser Ile Glu His
130 135 140

Ala Val Ser Ser Tyr Gln Thr Gly Thr Gln Thr Phe Asn Asn His Pro
145 150 155 160

Asn Phe Tyr Thr Asn Tyr Tyr Gln Ser Phe Ile Lys Asn Asp Asn Ile
165 170 175

Pro Tyr Ile Asn Gln Thr Asn Ile Phe Asp Asn Asn Ile Lys Asn Lys
180 185 190

Tyr Met Leu Asp Asp Lys Phe Gly Ser Thr Ser Leu Tyr Asn Asn Asn
195 200 205

Asn Asn Asn Asn Asn Asn Asn Glu Asn Asn Asn Asp Lys Tyr Leu Asn
210 215 220

Thr Tyr Tyr Ala Ser Pro Arg Gly Asn Gln Ile Tyr Asn Leu Phe Gln
225 230 235 240

Asp Ile Asn Asn Asn His His Asn Asn Asn Ile Asn Ser Tyr Ser Ile
245 250 255

His Ser Gly Met Thr Leu Tyr Asn Ile His Arg Cys Ile Cys Ile Cys
260 265 270

Leu Gly Val Lys Lys Glu Asp Thr Asp Asn Tyr Leu His Val Phe Ile
275 280 285

Leu Asn Asn Gly Asn Ile Tyr Gly Ser Gly Lys Lys Cys Ser Val Ser
290 295 300

Ile Ile Arg Lys Ile Gln Ile Asn Thr Asp Arg His Ile Thr Phe Lys
305 310 315 320

His Ile Ile Lys Thr Pro Leu Tyr Leu Tyr Lys Ser Lys Glu Asp Lys
325 330 335

Asn Lys Asn Asn Ser Asn Asn Asn Asn Asn Asn Asn Asn Ser Asn Asn
340 345 350

Asn Asn Asn Ser Asn Asn Asn Asn Asn Ser Asn Ser Asn Ser Asn Ser
355 360 365

Asn Asn Asn Thr Asn Ser Asn Ser Asn Ser Asn Ser Asn Ser Asn Asn
370 375 380

Asn Thr Asn Ser Asn Asn Asn Ser Asn Ser Asn Ser Asn Asn Asn Asn
385 390 395 400

Ser Asn Asn Asn Thr Thr Thr Asn Asn Ser Ser Ser Ser Asn Asn Ser
405 410 415

Asn Asn Asn Asn Tyr Tyr His Asn Asn Tyr Lys Asn Glu Lys Glu Leu
420 425 430

Asn Asn Ser Ser Ser Leu Glu His Ser Ser Ile Ile Met Asn Asn Asp

435 440 445

Asn Ile His Asn Asn Ile Asn Asn Asn His Ile Asn Asn Ile Thr Asp
450 455 460

Leu Asn Asn Met Asn Val Asn Gln Ser Asn Met Lys Glu Asn Asn Asn
465 470 475 480

Ile Ile Asp Tyr Met Asn Asn Asn Asn Asn Asn Asp Asn Tyr Ser Asn
485 490 495

Asn His Leu Asn Asn Cys Ile Asn Lys Leu Tyr Thr Asn Asn Ile Tyr
500 505 510

Phe Thr Glu Asp Ser Gln Lys Arg Asn Pro Leu Gln Thr Tyr Asn Thr
515 520 525

Ser Lys Asn Thr Asn Asn Phe Leu Asn Val Asn Asn Phe Thr Ser Ser
530 535 540

Tyr Asn Phe Pro Asn Ile Asn Asn Met Asp Ser Asn Ile Tyr Asn His
545 550 555 560

Thr Thr Cys Asn Asn Phe Asn Lys Asn Ile Asn Asn Asn Ile Asn Asp
565 570 575

Ile Ser Ile Asn Lys His Asn Asn Ile Phe Asn Asn Met Asn His Leu
580 585 590

Asn His Leu Asp Asn His Ser Tyr Ile Gln Asn Asn Leu Tyr Lys Asn
595 600 605

His Met Asn Val Asn Thr Asn Ile Leu Tyr Asn Asn Pro Ile Met Asn
610 615 620

Asn Ile Asn Asn Asp Gln Ile Asn Asn Leu Ser Ile Pro Asn Asn Lys
625 630 635 640

Asn Glu Asp Asn Asn Glu Ile Asn His Asp Asp Ser Asn Asp Asp Asp
645 650 655

Ser Asn Ser Ser His Ile Thr Leu Asn Lys Ser Asp Lys Asn Lys Asn
660 665 670

Tyr Phe Ala Leu Asn Pro Lys Tyr Gln Asn His Gln Asn His Asn Ile
675 680 685

Asn Asn Asn Ile Gln Asn Asn Leu Asn Glu Gln Ile Lys Glu Lys Asn
690 695 700

Asp Gln Gln Asn His Asn Ile Lys Glu Ile Lys Asn Lys Glu Leu Leu
705 710 715 720

Asn Asp Thr Ile Ser Ser Ile Glu Asp Thr Asn Asp Asn Ser Tyr Ser
725 730 735

Lys Tyr Ile Thr Ser Ser Asp Ile Ser Gln Asn Asn Thr Leu Asn Ser
740 745 750

Phe Gln His Asn Lys Glu Ile Ser Val Asn Phe Met Tyr Asn Asn Ile
755 760 765

Ile Leu Asp Asn Asn Asn Asn Ile Asn Asp Asp Asn Asn Asn Asn Asn
770 775 780

Asn Tyr Phe Cys Ile Pro Cys Gly Tyr Asn Thr Lys Glu Tyr Lys Tyr
785 790 795 800

Asn Ile Tyr Asn Thr Tyr Asn Tyr Pro Asn Asn Ala Asn His Ile Tyr
805 810 815

Asn Asn Met Asn Ile Ser Tyr Asn Asn Ser Ala Tyr Asn Asn Asn Tyr
820 825 830

Val Thr Tyr Asn Asn Phe His Asn Ser Tyr His Asn Asn Tyr Ile Leu
835 840 845

His Asn Asn Phe His Asn Pro Tyr Asn Ile Tyr Asp Asn Ile Gln Asn
850 855 860

Thr Glu Gln Lys Lys Leu Tyr Asn Ile Tyr Gln Asn Asp Glu Arg Gln
865 870 875 880

Asn Asn Ser Phe Asn His Ile Asn Thr Asp Pro His Lys Val Val Asn
885 890 895

Ser Asn Asn Phe Leu Pro Ile Asn Thr Phe His Tyr Asn Asn Asn Leu
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Asn His Asn Ile Leu Thr Glu Ser Asn Asn Leu Asn Arg Lys Asn Glu
915 920 925

Asn Asp Asn Ile Pro Ser Ser Tyr Ser Gln Ile His Asn His Gln Ile
930 935 940

Cys Lys Lys Val Glu Glu Tyr Thr Tyr Asn Ser Ile Asn Gln Asn Thr
945 950 955 960

Asn Asn Phe Asn Asn Asn Val Met Met Leu Met Asn Thr Ser Asn Asn
965 970 975

Ile Pro Leu Asp Asn Asn Thr Tyr Asn Ser Asn Lys Asn Lys Ile Ile
980 985 990

Tyr Lys His Ile Ile Asn Asp His Ile Asn Gln Lys Asp Asn Asn Val
995 1000 1005

Glu Tyr Glu Asn Leu Asn Asn Ser Cys Asp Asn Thr Gln Asn Lys
1010 1015 1020

Glu Thr Phe Cys Asn Gln Asp Leu Ile Asn Ser Ser Asn Ile Asn
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Asn Asn Ile Ser Ser Tyr Thr Phe Gln Asn Asn Asn Asp Phe Tyr
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Thr Lys Lys Lys Ser Met Gln Tyr Asn His Asp Asn Ile Tyr Lys
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Ile Asn Thr Thr Ser Glu Asn Val Gly Ser Pro His Thr Asn Asn
1070 1075 1080

Lys Thr Ser Ile Tyr Asn His Lys Lys Gly Gly Tyr Glu Gln His
1085 1090 1095

Thr Glu Gln Asn Asn Glu Gln Asn Asn Glu Gln Asn Ser Glu Gln
1100 1105 1110

Asn Ile Glu Gln Asn Ile Glu Gln Asn Ile Glu Gln Asn Val Ala
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Gln Asn Val Ala Gln Asn Val Ala Gln Asn Val Glu Gln Asn Val
1130 1135 1140

Glu Gln Asn Val Ala Gln Asn Val Glu Gln Asn Val Glu Gln Asn
1145 1150 1155

Val Glu Gln Lys Ala Glu Gln Asn Ser Asn Asn Glu Ser Ile Lys
1160 1165 1170

Thr Asn Thr Val Glu Thr Phe Lys Arg Asn Lys Asn Gln Ile Thr
1175 1180 1185

Asn Ser Asn Asn Val Ile Ser Lys Gln Gln His Asp Thr Asn Asn
1190 1195 1200

Ile Leu Asn Asn Ile Asn Ile Asn Ile Lys Glu Asn Ile Asn Arg
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His Lys Ile Asn Glu Phe Gln Trp Glu Lys Ser Asn Lys Ile Asp
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Ile Glu Lys Asn Asn Cys Leu Thr Thr Lys Tyr Asp Lys Asp Asn
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Asp Asn Glu Asn Asp Asn Glu Asn Asp Asn Thr Tyr Asn Lys Asn
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Asn Asp Ile Val Ile Cys Asn Asn His Asn Asn Ser Ser His Val
1265 1270 1275

Gln Lys Asn Tyr Tyr Asn Met Asn Glu Ser Met Ile Asn Glu Asn
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Asn Ile Ile Ile Thr Glu Gly Glu Asn Leu Met Asn Ser Thr Glu
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Glu Tyr Phe Thr Asn Glu Leu Ile Lys Lys Asp Ser Leu Glu Lys
1310 1315 1320

Asn Lys Ser Asp Thr Lys Phe Leu Ile Lys Leu Asn Asn Glu Ile
1325 1330 1335

Lys Lys Glu Glu Glu Lys Lys Asp Asn Ile Asn Ile Phe Ile Asn
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Asn Asn Ile Tyr Glu Leu Lys Glu Ile Asn Gly Asn Lys Asn Arg
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Ser Asp Tyr Phe His Asn Thr Lys Asp Asp Lys Glu Asn Ile Thr
1370 1375 1380

Asn Val Ser Ser Asn Asn His Leu Ser Val Pro Leu Asn Lys Tyr

1385 1390 1395

Asn Asp Glu Asp Lys Gln Leu Ile Lys Gln Met Asn His Ala Ser
1400 1405 1410

Asn Met Asn Phe Ile Tyr Asp Tyr Asn Tyr His Asn Asn Tyr Ser
1415 1420 1425

Ser Thr Asn Ser Gln Gln Leu Ile Lys Asn Asn Thr Glu Asn Leu
1430 1435 1440

His Ser Phe Lys Asn Glu Thr His Ser Thr Tyr Val Lys Tyr Ile
1445 1450 1455

Lys Ser Glu Ile Asn Asn Met Asn Asn Ser Ile Gly Val Pro Thr
1460 1465 1470

Lys Lys Asn Asp Tyr Met Tyr Thr Asn Tyr Leu Asn Met Glu His
1475 1480 1485

Ile Lys Met Asn Asn Met Glu Lys Glu Ile Ile Lys Lys Gly Asn
1490 1495 1500

Asp Asn Glu Ile Lys Gly Gln Arg Ile Gln Val Glu His Asp Arg
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Asp Val His Tyr Asn Thr Thr Gln Glu Asn Asn Ile Ile Asn Asn
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Gln Asn Pro Gln Thr Asn His Asp Gly Asp Met Asn Ile Asn Ile
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Asn Ser Asn Lys Phe Met Thr Pro Thr Thr Leu Lys Glu Lys Tyr
1550 1555 1560

Gln Asn Asn Ile Asn Thr Asn Glu Gln His Asn Lys Asn Glu Glu
1565 1570 1575

Asn Lys Asn Lys Asn Val Ile Asn Asn Thr Ser Gln Met Ile Asn
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Asp Asn Asn Val Ile Gln Asn Asp Ile Asn Asn Met Asn Asn Asn
1595 1600 1605

Glu Asn Glu Asn Glu Asn Glu Asn Leu Tyr Ile Asn Val His Thr
1610 1615 1620

Gln Tyr Lys Ser Asp Asn Ile Leu Ser Cys Glu Lys Asn Phe Ile
1625 1630 1635

Thr Leu Lys Asn Asn Asn His Asn Asn His Asn Asn Asn Asn Asn
1640 1645 1650

Tyr Tyr Tyr Tyr Tyr Ile Asn Asn Asp Asn Ile His Leu Asn Asn
1655 1660 1665

Ser His Ile Asp Ile Met Lys Thr Asn Asn Ile Asn Lys Asp Met
1670 1675 1680

Thr Thr Asn Ser Thr Pro His Phe Lys His Asn Ile Ile Ser Asn
1685 1690 1695

Asp Cys Ser Pro Asn Asn Ile Asn Gln Asn Ile Phe Val Asp Pro
1700 1705 1710

Asn Lys Tyr Ile Tyr Asn Asn Ile His Thr Asn Tyr Asn Ala Tyr
1715 1720 1725

His Glu Glu Ser Leu Gln Val Val Gly Asn His Asn Ser Ser Ser
1730 1735 1740

Leu Leu Arg Asn Ile Asn Glu Ser Phe Ser Asn Gln Tyr Asp Asn
1745 1750 1755

Lys Lys Asn Leu Glu Ala His His Ile Asp Asp Asp Lys Asn Lys
1760 1765 1770

Glu Ala Phe His Asn Asp Asp Asp Lys Asn Lys Glu Ala Phe His
1775 1780 1785

Asn Val Asp Asp Lys Asn Lys Glu Thr Phe His Asn Asp Asp Asp
1790 1795 1800

Lys Asn Lys Glu Ala Leu His Asn Asp Asp Asp Lys Asn Lys Glu
1805 1810 1815

Ala Leu His Asn Asp Asp Asp Lys Asn Val Glu Ala Tyr His Asn
1820 1825 1830

Asp Asn Tyr Asn Asp Asn Tyr Asn Asn Asn Tyr Tyr Phe Asp Gly
1835 1840 1845

Asn Asn Asn Met Gln Asp Glu Ser Phe Tyr Ser Asn Asn Ser His
1850 1855 1860

Ala Glu Tyr Asn Gln Ser Asn Ile Glu Tyr Ile Ser Asn Tyr Asp
1865 1870 1875

Lys Asn Tyr Ser His Ile Gln Gln Tyr Thr Asn Gly Phe Cys Tyr
1880 1885 1890

Thr Asn Asn Asn Gln Tyr Ile Asn Asn Thr Glu Leu Thr Asn Asn
1895 1900 1905

Ser Ser Tyr Ile Tyr Asn Asn Ser Tyr Met Asn Asn Asn Thr Tyr
1910 1915 1920

Ser Phe Asn Lys Glu Tyr Ser Asp Asn Asn Met Cys His His Lys
1925 1930 1935

Asn Asp Asn Ile His Met Ile Asn Asp Val Ala Thr Lys Leu Asn
1940 1945 1950

Gln His Pro Met Asn Met Tyr Asn Ser Asn Asn Asn Asn Ile Ile
1955 1960 1965

Tyr Asn Asn Asn Asn Asn Gln Ile Tyr Asp Asn Asn Ile Asn Asn
1970 1975 1980

Met Tyr Asn Asp Tyr Tyr Asn Tyr Asn Asn Asn Asn Met Tyr Asn
1985 1990 1995

Asn Tyr Tyr Asn Tyr Asn Asn Asn Asn Asn Met Tyr Asn Asn Tyr
2000 2005 2010

Tyr Asn Tyr Ser Asn Lys Asn Phe Tyr Met Asn Glu Lys Tyr Thr
2015 2020 2025

Glu Gly Ala Thr Asn Phe Met Asn Ile Asp Asp Met Lys Asp Ala
2030 2035 2040

Gly Asn Glu Asn Asn Met His Ile Leu Asn Asn Asn Ser Ile Asn
2045 2050 2055

Gln Thr Tyr Tyr His Ser Lys Ile Lys Asn Asn Asn Asn Asn Asp
2060 2065 2070

Asp Asp Asp Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asp Asn
2075 2080 2085

Asn Asp Asn Asn Asn Ile Met Met His Asn Asn Tyr Gln Pro Phe
2090 2095 2100

Leu Tyr Glu Asn Gln Tyr Asn Lys His Ile His Met Met Asn Gln
2105 2110 2115

Gln Ile Gln Lys Glu Thr Asn Thr Ser Phe Lys His Ile Thr Cys
2120 2125 2130

Asn Gln Lys Phe Ile Glu Asn Asn Lys Ile Asn Ile Ser Asn Asp
2135 2140 2145

Gln Asn Val Thr Asn Met Pro Ile Leu Tyr Ser Met Asn Lys Glu
2150 2155 2160

Gln Tyr Ile Asn Ile Ser Asn His Asn Asn Gly Cys Asn Tyr Asp
2165 2170 2175

Asn Ile Asn Ser Ile Asn Val Tyr Glu Asn Asn Asn Glu Tyr Ile
2180 2185 2190

Ala Pro Lys Asn Met Leu Tyr Lys Ser Glu Glu Lys Glu Asn Leu
2195 2200 2205

Tyr Asn Ser Ser Ser Ile Tyr Asn Gln Asn Tyr Glu Gln Lys Tyr
2210 2215 2220

Ile Asn Tyr Met Asn Asn Ala Ser Tyr Ile Met Asn Asn Asn Met
2225 2230 2235

Asn Asp Tyr Thr Asn Asn Tyr Asn Val Gln Asn Phe Arg Thr Phe
2240 2245 2250

Lys Asn Asn Val Phe Gln Gln Pro Leu Ser Tyr Ser Asn Gly Ser
2255 2260 2265

Glu Ala Met Leu His Ala Ser Glu Phe Asn Gln Gly Ile Asn Lys
2270 2275 2280

Glu Asn Phe Gln Gly Glu Tyr Val Ser Asn Leu Val Asn Ser Tyr
2285 2290 2295

Lys Asp Asn Val Asn Asn Val Glu Gly Val Leu Gly Ile Lys Lys
2300 2305 2310

Asp Lys Glu Asn Asp Asn Asn Glu Glu Glu Asn Asp Glu Glu Glu
2315 2320 2325

Asn Asp Glu Glu Glu Asn Asp Glu Glu Glu Asn Asp Glu Glu Glu
2330 2335 2340

Asn Asn Glu Glu Glu Asn Lys Glu Ala Gln Asn Asn Glu Glu Glu
2345 2350 2355

Asn Asn Asn Gly Asp Asn Asn Asn Gly Asp Asn Asn Asn Asn Gly
2360 2365 2370

Asp Asn Asn Asn Asn Gly Asp Asn Asn Asn Asn Gly Asp Asn Asn
2375 2380 2385

Asn Asn Gly Asp Asn Asn Asn Asn Asn Ile Phe Tyr Asn Met Glu
2390 2395 2400

Gly Ser Gln Lys Ile Cys His Asp Asp Ile Thr Leu Asn Glu Cys
2405 2410 2415

Leu Asn Ser Ile Asp Ile Asn Glu Gly Glu Lys Lys Thr Phe Glu
2420 2425 2430

Glu Asn Lys Ser Ser Phe Ser Met Leu Tyr Leu Phe Gly Lys Val
2435 2440 2445

Lys Phe Tyr Ile Ser Ile Ile Asp Ile Ile His Asn Lys Thr Asn
2450 2455 2460

Ser His Asp Leu Leu Trp Val Pro Arg Cys Cys Asn Gly Ser Tyr
2465 2470 2475

Gly Thr Phe Leu Lys Tyr Asn Tyr Ser Asn Met Asn Glu Ile Asn
2480 2485 2490

Lys Tyr Thr His Asp Glu Gly Ile Asp Ile Asp Ser Ile Asn Leu
2495 2500 2505

Lys Leu Met Glu Thr Arg Phe Ser Lys Asn Val Ala Ser Ser Arg
2510 2515 2520

Thr Thr Lys Arg Lys Arg Met Ile Asp Ile Asp Lys Thr Val Leu
2525 2530 2535

His Tyr Tyr Lys Glu His Ile Ser Glu Phe Phe Asn Asp Lys Asn
2540 2545 2550

Lys Ile Ile Lys Leu Thr Lys Lys Leu Cys Lys Tyr Lys Lys Lys
2555 2560 2565

Arg Lys Phe Asn Asp Thr Gln Lys Lys Gly Thr Tyr Lys Asp Glu
2570 2575 2580

Lys Asp Tyr Asp Asn Tyr Asp Val Leu Pro Asn Gly Asp Glu Gln
2585 2590 2595

Asn His Glu Asn Lys Lys Gln Glu Asp Asn Asn Asn Asn Asn Asp
2600 2605 2610

Asp Asn Asn Asn Lys Asn Lys Asn Asn Asp Asp Asp Asn Asn Asn
2615 2620 2625

Asn Asn Asn Asn Asn Asn Asn Asn Asn Asp Asn Asn Asn Lys Asn
2630 2635 2640

Asn His Asn Asn Asp Asn Asn Asn Asn Asp Asn Asn Asn Lys Asn
2645 2650 2655

Asn His Asn Asn Asn Asn Asn Asp Asn His Lys Asn Asn Ser Asn
2660 2665 2670

Asn Lys Ala Lys Gly Lys Asn Met Gly Lys Gly Lys Lys Gln Thr
2675 2680 2685

Pro Asn Arg Met Asn Asn Thr Lys Asn Val Gln Asn Gly Lys Asn
2690 2695 2700

Thr Lys Asn Ile Asn Asn Ile Lys Asn Ile Ser Asn Met Ser Asn
2705 2710 2715

Ile Glu Ser Ile Asn Ser Met Thr Ser Ile Lys Ser Val Asp Gly
2720 2725 2730

Glu Asn Arg Met Asn Asn Thr Ile Asn Met Asn Gly Met Asn Lys
2735 2740 2745

Thr Glu Ser Ile Asn Asn Ile Glu Ile Thr Gln Asn Met Asn Thr

2750 2755 2760

Ile Asn Ser Ile Asn Asn Ile Asn Gly Ile Asn Asn Ile Asn Gly
2765 2770 2775

Ile Asn Asn Val Asn Gly Ile Asn His Thr Asn Gly Ile Asn His
2780 2785 2790

Thr Asn Gly Ile Asn Asn Ile Asn Thr Met Asn Asn Met Asn Asn
2795 2800 2805

Met Asn Asn Ile Asn His Ile Asn Asn Ile Asn Asn Met Asn Asn
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Met Asn Asn Met Asn Arg Ile Asn Ser Leu Asn Asn Lys Asn Asn
2825 2830 2835

Ile Asn Pro Ile Asn Gln Tyr Asn Asp Glu Lys Gln Asn Leu Leu
2840 2845 2850

Asn Ser His Leu Gln Phe Asn Gln Val Asn Tyr His Asn Asn Leu
2855 2860 2865

Val Asn Gly Leu His Lys Asn Asn Phe Leu Ser Asn Asn Asn Tyr
2870 2875 2880

Ile Asn Thr Thr Asp Ile Asn Gly Asn Asn Met Ile Ser His Asn
2885 2890 2895

Asp His Met Asn Asn Lys Leu Tyr Ser Asn Ile Asn Asn Asn Tyr
2900 2905 2910

Tyr Tyr Asn Arg Ala Asn Asn Glu Ile Pro Asn Asn Asn Ser Asn
2915 2920 2925

Asn His Asn Asn Asn Phe Asn Ile Tyr Glu Ser Lys Tyr Gln Thr
2930 2935 2940

Met Ile His Asn Asn Asn Ile Gly Gln Asp Leu Lys Gln Gln Ile
2945 2950 2955

Asn Asn Tyr Asn Glu Asn Thr Ser Ser Asn Asn Asn Leu Ser Ile
2960 2965 2970

Ser Gln Leu Leu Glu Gly Asn Thr Asn Phe Ile Asn Ile Ser Asn
2975 2980 2985

Thr Phe Ile Asn Thr Asn Tyr Ser Asn Asp Phe His Gln Thr Asn
2990 2995 3000

Asp Leu Leu Val Asn His Asn Asn Ile Asp Leu Lys Tyr Leu Ser
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Asp Asn Ile Asn Thr Asn Thr Tyr Asn Glu Gln
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Ala Phe Leu Leu Ile Thr Phe Leu Met Ile Asn Leu Asn Glu Glu Ser
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Leu Glu Leu Ser Gln Ala His Arg Glu Asn Gly Lys Lys Ala Leu Val
35 40 45

Val Ala Ile Ile Leu Tyr Val Ile Phe Leu Val Leu Leu Phe Ile Tyr
50 55 60

Lys Ala Tyr Lys Asn Lys Arg Lys Leu Tyr Thr Asn Phe Phe Met Lys
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Lys Arg Asn Ala Pro Lys Tyr Val Gln Leu Ala Ser Thr Tyr Leu Ser
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Ala Ser Asp Glu Tyr Glu Gln Tyr Glu Leu Asn Lys Ile
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Glu Ser Asn Glu Arg Tyr Gln Asp Pro Gln Asn Tyr Glu Leu Ser Lys

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Lys Ala Val Ile Phe Thr Pro Ile Tyr Tyr Phe Asp Gly Asn Ser Trp
35 40 45

Thr Ala Leu Glu Arg Leu Leu Ser Leu Lys Lys Thr Ile Phe His Asp
50 55 60

Asn Arg Leu Val Thr Leu Cys Pro Val Glu Asn Asn Ile Thr Pro Ile
65 70 75 80

Glu Leu Glu Ala Ser Ile Ser Gly Lys Tyr Asp Ile Lys Val Tyr Arg
85 90 95

His Cys Glu Tyr Ile Leu Cys Ile Glu Gly Glu Gln Lys Ile Leu Ile
100 105 110

Lys Ile Pro Val Thr Lys Asn Ile Ile Thr Trp Asn Ser Glu Gln Arg
115 120 125

Leu Pro Leu Leu Pro Lys Thr Trp Lys Pro Thr Ile Phe Leu Leu Asn
130 135 140

Glu Ser Asn Ile Phe Leu Arg Phe Ile Pro Asp Lys Cys Leu Val Ile
145 150 155 160

Ser Gln Val Ser Asn Ser Asp Ser Tyr Lys Val Asn Cys Ile Asn Phe
165 170 175

Ser Glu Gly Phe Cys Cys Cys His Pro Ile Asn Asn Leu Ala Leu Leu
180 185 190

Tyr Gly Glu Tyr Gln Gln Asn Gln Glu Ser Lys Ile Met Lys Leu Pro
195 200 205

Lys Leu Pro Ile Ser Asn Gly Lys Tyr Asn Tyr Phe Ile His Phe Phe
210 215 220

Thr Trp Gly Thr Met Phe Val Pro Lys Tyr Phe Glu Leu Ser Arg Gly
225 230 235 240

Pro Leu Cys Asn Phe Lys Lys Asn Ile Ile Ala Leu Leu Ile Ile Pro
245 250 255

Pro Lys Ile His Ile Ser Ile Glu Leu His Ser Ser Ser Pro Val Val
260 265 270

Cys Ser Met Glu Tyr Lys Lys Asp Phe Leu Ile Thr Ala Arg Lys Pro
275 280 285

Asn Ile Thr Asp Ile Glu Ile Tyr Thr Ile Ile Gln Asp Gln Leu Ile
290 295 300

Lys Tyr Asp Phe Ser Tyr Asp Leu Arg Leu Asn Lys Glu Asn Ala Ser
305 310 315 320

Ile Ser His Leu Asn Ile Pro Ile Gly Phe Lys Ile Cys Asn Glu Glu
325 330 335

Lys Glu Lys Lys Lys Lys Asn Ser Ser His Ile Cys Lys Trp Thr Phe
340 345 350

Ile Glu Thr Lys Asp Gln Arg Thr Leu Asn Arg Ser Gly Asn Ser Ser
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Ser Glu His Ile Met Ser Gln Asp Leu Ala Cys Ile Phe Asp Ala Glu
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Lys Ala Met Ile Cys Cys Leu Leu Ser Asn Ile
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Lys Asp Arg Asn Asn Asn Asp Asp Leu Gly Val Met His Asn Tyr Ala
35 40 45

Asp Asp Ser Glu Trp Arg Glu His Asn Lys Lys Asp Arg Met Thr Ser
50 55 60

Leu Lys Asn Glu Leu Asn Glu Gln Leu Ile Tyr Thr Tyr Tyr Asn Asn
65 70 75 80

Phe Asn Asn Asn Tyr Glu Tyr Tyr Asn Lys Ser Thr Glu Lys Leu Lys
85 90 95

Glu Lys Asn Asn Glu Asp Glu Tyr Asn Glu Glu Gln Glu Tyr Glu Pro
100 105 110

Thr Ala Asn Leu Leu Gln Asp Lys Asn Lys Ile Asn Asp Met Asn Asn
115 120 125

Phe Tyr Asn Asn Phe Asn Lys Asn Ser Leu Phe Asn Tyr Gln Asn Phe
130 135 140

Gln Asn Ala Asp Lys Asn Phe Leu Tyr Leu Leu Asn Lys Lys Asn Lys
145 150 155 160

Asn Asn Ser Thr Asn Glu Asn Ile Leu Val Asp Glu Phe Lys Lys Leu
165 170 175

Lys Asn His Val Leu Phe Leu Gln Met Met Asn Val Asn Leu Gln Lys
180 185 190

Gln Leu Leu Thr Asn His Leu Ile Asn Thr Pro Lys Ile Met Pro His
195 200 205

His Ile Ile Ile Asn Asn Lys Thr Glu Val Ser Ser Asn Ala Val Ser
210 215 220

Glu Ile Gln Asn Asn Lys Asp Lys Lys Lys Asn Gly Thr Met Tyr Ile
225 230 235 240

Leu Leu Lys Lys Ile Leu Ser Ser Arg Phe Asn Gln Met Ile Phe Val
245 250 255

Ser Ser Ile Phe Ile Ser Phe Tyr Leu Ile Asn Lys His Trp Gln Arg
260 265 270

Ala Leu Lys Ile Ser Gln Leu Gln Lys Lys Ile Asn Ser Asn Phe Leu
275 280 285

Leu Lys Ser Val Arg Leu Phe Glu Glu Ser Leu Gly Ile Arg Lys Asn
290 295 300

Lys Tyr Ile
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Val Asp Val Cys Asn Ile Leu Lys Glu Asn Asn Thr Tyr Lys Gln Lys
35 40 45

Lys His Ile Ser Ile Asn Ile Asn Arg Lys Cys Ala Ser Tyr Asn Asn
50 55 60

Ile Tyr Tyr Ile Asn Asn Asp His Pro Gly Leu Gly Lys Asn Ile Ser
65 70 75 80

Tyr Tyr Gln Asn Lys Asp Asn Met Gln Leu Lys His Phe Phe Asn Ser
85 90 95

Asn Lys Ile Asn Ile His Asp Asn Lys Ile Lys Thr Thr Gln Ser Tyr
100 105 110

Ser Tyr Tyr Glu Pro Leu Arg Tyr Pro Ala Phe Lys Met Ser Asp Lys
115 120 125

Ile Lys Ser Glu Thr Asn Glu Leu Lys Lys Met Asp Thr Lys Lys Asp
130 135 140

Val His Met Lys Asp Ile His Pro Lys Asn His Lys Ile Ser Lys Asn
145 150 155 160

Asp Asp Leu Gly Asn Asn Asn Ile Asp Asn Asn Asn Asn Asn Asp Asp
165 170 175

Asn Asn Asn Ser Asn Asn Asn Asn Asn Asn Asn Ile Lys Cys Val Ser
180 185 190

Asn Arg Ser Thr Ser Asn Lys His Ile Asn Arg Arg Asn Met Cys Ile
195 200 205

Phe His Asn Lys Ile Asn Lys Lys Glu Lys Asn Ile Asn Glu Gln Gly
210 215 220

Glu Lys Asn Glu His Ser Lys Ile Asp His Lys His Phe Gly Asn His
225 230 235 240

Ile Leu Lys Asp Val Lys Asn Lys Lys Lys Ser Asn Asn Ile Ile Pro
245 250 255

Leu Leu Tyr Glu Glu Asn Lys Asn Asn Ile Asn Ile Asn Ser Lys Asn
260 265 270

Gly Asn Ser Asn Asn Leu Glu His Glu His Val Gln Glu Lys Pro Ala
275 280 285

Arg Phe His Lys Lys Lys Arg Lys Lys Lys Gln Asn Lys Leu Ala Gly
290 295 300

Asn Lys Ile Lys Asn Asn Gly Lys Asn Glu Glu Val Lys Gln Ser Ser
305 310 315 320

Val Ile Glu Met Glu Lys Val Asn Tyr Leu Asp Asp Lys Val Asn Gly
325 330 335

Asn Val Glu Glu Lys Lys Lys Lys Lys Lys Lys Asn Lys Asn Lys Asp
340 345 350

Lys Asp Lys Lys Arg Asp Glu Glu Lys Glu Glu Asp Lys Asn Lys Asp
355 360 365

Lys Asp Lys Asp Lys Asp Lys Asn Asn Asn Asn Asn Asn Asn Asn Asn
370 375 380

Asn Asn Asn Asn Lys Asn Asn Asn Lys Asn Lys Asn Lys Lys Lys Lys
385 390 395 400

Asn Lys Ile Asn Asn Asn Asn Ile Asn Lys Asn Lys Asp Lys Asp Met
405 410 415

Ser Lys Asn Lys Arg Lys Asn Lys Asn Lys Asn Glu Val Val Glu Asp
420 425 430

Asn Lys Asn Lys Gln Tyr Leu Glu Lys Lys Glu Asn Asn Ile Asn Glu
435 440 445

Ile Pro Lys Glu Val Met Tyr Ile Pro Ile Glu Glu Arg Cys Lys Ser
450 455 460

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Ile Val Ser Ser Ser Asp Glu Glu Asn Leu Tyr Tyr Glu Lys Pro Tyr
465                 470                 475                 480

Glu Glu Val Glu Asn Tyr Phe Glu Phe Ile Glu Asn Lys Asn Leu Ile
                485                 490                 495

Asn Pro Ser Asp Ile Thr Asn Glu Val Lys Phe Ile Leu His Met Thr
            500                 505                 510

Leu Leu Thr Leu Tyr Lys Asp Gln Ile Lys Pro Ser Tyr Gly Lys Ile
        515                 520                 525

Lys Lys Arg Leu Thr Cys Phe Asn Glu Asn Leu Glu Ile Lys Tyr Asn
    530                 535                 540

Phe Leu Asn Ile Tyr Ala Ser Leu Arg Asn Glu Tyr Ile Val Val Arg
545                 550                 555                 560

Thr Lys Arg Asn Asn Ile Phe Val Leu Leu Arg Glu Thr Pro Lys Trp
                565                 570                 575

Phe Leu Gly Trp Val Lys Thr Arg Cys Phe Lys Asn Ser Tyr Pro Lys
            580                 585                 590

Lys Val Trp Lys Lys Leu Ile Glu Tyr Phe Leu Asn Met Thr Lys Ser
        595                 600                 605

Asn Met Asn Asn Asn Leu Tyr Val Ser Met Tyr Ile Pro Phe Ile Lys
    610                 615                 620

Lys Phe Tyr Asp Lys Arg Phe Ile Phe Tyr Leu Asn Glu Lys Asp Asn
625                 630                 635                 640

Glu Lys Asn Lys Cys Tyr Glu Lys Ile Tyr Asn Phe Ser Phe Leu Ser
                645                 650                 655

Phe Asp Met Asn Glu Gln Lys Lys Lys Arg Asn Asn Phe Asn Val Leu
            660                 665                 670

Phe Tyr Ile Tyr Asn Met Tyr His Asn Asn Phe Ser Tyr Phe Ser Gln
        675                 680                 685

Cys Asn Asp Tyr Tyr Ile Lys Asn Val Glu Lys Asn Phe Leu Leu Tyr
    690                 695                 700
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Tyr Thr Tyr Ile Phe Phe Asn Tyr Asp Lys Asn Asp Leu Asn Asn Asn
705 710 715 720

Asn Ser Asn Ile Asp Leu Ser Lys Lys Asn Tyr Leu Cys Glu Asp Lys
725 730 735

Asn Lys Asp Thr Thr Thr Thr Ser Asn Asn Asn Asn Asn Asn Asn Asn
740 745 750

Asn Asn Asn Asn Asp Asn Asn Asn Asn Asn Asp Asn Asn Asn Asn Ser
755 760 765

Ser Ser Cys Ser Asn Asn Asn Asn Ser Ser Ser Ser Ser Ser Ser Tyr
770 775 780

Asn Asn Asn Cys Asn Asn Tyr Thr Ser Leu Tyr Val Glu His Leu Phe
785 790 795 800

Asn Asp Lys Lys Glu Asn Ile Leu Gln Thr Asp Glu Ile Ile Lys Tyr
805 810 815

Asp Ile Thr Lys Asn Leu Ile Asn Glu Glu Asn Asn Ile Asp Thr Thr
820 825 830

Asn Met Phe Asp Ile Phe Asn Asn Asp Ile Tyr Glu Val Ala Asp Ile
835 840 845

Leu Lys Lys Lys Asn Phe Pro Ile Leu Lys Asp Tyr Ser Leu Gly Lys
850 855 860

Ile Ala His Ile Ile Tyr Leu Cys Leu Tyr Asn Gly Leu Leu Leu Glu
865 870 875 880

Glu Asn Gln Lys Ile Ile Pro Ala Cys Ser Ser Lys Asn Ile Ile Ser
885 890 895

Ser Ile Phe Tyr Ile Lys Asn Lys Asn Ser Tyr Leu Tyr Asp Asn Tyr
900 905 910

Ser His Leu Asn Gln Asn Phe Tyr Cys Asp Asp Asn Asn Ile Ser Thr
915 920 925

Tyr Gly Tyr Asp Tyr Asn Glu Ser Thr Ser Ile Asn Leu Met Thr Lys
930 935 940

Glu Tyr Asp Asp Lys Met Asp Ser Phe Leu Asn Val Tyr Glu Asn Phe
945 950 955 960

Leu Lys Asn Glu Glu Gly Leu Phe Phe Ser Lys Lys Lys Asn Asn Lys
965 970 975

Cys Asp Val Asn Val Ser Leu Asn Lys Cys Thr Glu Glu Phe His Ile
980 985 990

Pro Ala Ile Thr Asn Leu Glu Glu Ala Lys Phe Lys Ile Glu Arg Leu
995 1000 1005

Leu Lys Ser Ser Tyr Lys Lys Cys Ile Tyr Leu Leu Phe Phe Arg
1010 1015 1020

Glu Lys Phe Leu Lys Lys Tyr Lys Gln Asn Ile Asn Pro Leu Ile
1025 1030 1035

Phe Gly Tyr Asn Ser Leu Ile Glu Phe Leu Phe Tyr Gly Cys Arg
1040 1045 1050

Glu Val Cys Lys Ile Tyr Ile Leu Asn Asn Asn Leu Leu Ile Val
1055 1060 1065

His Leu Ser Tyr Asp Ile Ala Lys His Ile Asn Asn Asn Asn Glu
1070 1075 1080

Lys Glu Lys Asp Lys Glu Lys Glu Lys Glu Lys Glu Lys Glu Asn
1085 1090 1095

Val Ile Glu Glu Phe Tyr Tyr Ser Asp Tyr Cys Tyr Asn Lys Thr
1100 1105 1110

Glu Asn Asn Asn Asn Lys Phe Asn Asn Ser Ser Leu Glu Val Cys
1115 1120 1125

Thr Ile Met Lys Asp Asn Ala Lys Lys Lys Asn Ser Phe Phe Ile
1130 1135 1140

Thr Tyr Ser Tyr Trp Lys Tyr Met Ser Lys Lys Glu Lys Gln Asn
1145 1150 1155

Asp Ile Leu Asp Asn Val Ser Phe Leu Lys Gly Glu Gln Asn Tyr
1160 1165 1170

Ile Phe Ser Asp Asp Ile Trp Lys Ile Asn Lys Cys Ser Phe Asp
1175 1180 1185

Lys Thr Asn Pro Ile Gln Gln Ser Gly Lys Asp Ile Pro Leu Tyr
1190 1195 1200

Tyr Lys Asn Met Lys Lys Ile Asn Thr Gly Ile Phe Asn Met Pro
1205 1210 1215

Asn Leu Val Gln Ile Asn Asn Tyr Asp Phe Glu Phe Phe Ser Thr
1220 1225 1230

Cys

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<212> PRT
<213> Plasmodium falciparum

<400> 15

Met Tyr Asp Ala Asp Lys Cys Glu Ala Ile Leu Val Leu Asp Ile Pro
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Gly Phe Lys Ile Glu Asp Ile Asp Val Glu Ile Gly Glu Gly Met Leu
20 25 30

Thr Val Ala Gly Pro Arg Ser Gln Thr Glu Leu Phe Glu Thr Tyr Gly
35 40 45

Asp Ser Leu Val Leu His Ala Lys Glu Arg Glu Val Gly Tyr Phe Lys
50 55 60

Arg Ile Phe Lys Leu Pro Asn Asn Ile Leu Asp Asp Thr Ala Lys Ala
65 70 75 80

Thr Tyr Lys Asn Gly Asn Ile Tyr Ile Tyr Ile Tyr Ile Tyr Ile Tyr
85 90 95

Phe Leu Gln Ile
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<210> 16
<211> 253
<212> PRT
<213> Plasmodium falciparum

<400> 16

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Met Ile Lys Gln Asn Ile Lys Tyr Thr Gln Ile Ile Ser Ile Asp Asn
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Ile Leu Asn Lys Ile Ala Asp Pro Ile Leu Ile Gly Phe Ser Ser Ser
            20                  25                  30

Phe Asn Cys Asp Ile Ala Asn Lys Ala Val Gln Arg Glu Asp Glu Glu
        35                  40                  45

Ser Met Gly Val Phe Cys Leu Lys Glu Lys Val Lys Asn Lys Ile Asn
    50                  55                  60

Lys Lys Tyr Asn Lys Lys Asn Lys Asp Asn Ile Phe Lys Asn Asp Asn
65                  70                  75                  80

Asn Thr Phe Ser Val Cys Glu Tyr Thr Glu Leu Asn Glu Cys Ile Leu
                85                  90                  95

Asn Asn Lys Glu Leu Phe Lys Tyr Gly Asn Ile Cys His His Ile Ile
            100                 105                 110

Thr Val Asp Phe Leu Lys His Ile Val Lys Asn Arg Ile Tyr Asn Lys
        115                 120                 125

Leu Lys Leu His Lys Ile Ile Arg Lys Lys Gln Tyr Thr Asp Ile Pro
    130                 135                 140

Ser Leu Ile Asn Asp Asn Asn Glu His Leu Ile Asn Ser Lys Val Phe
145                 150                 155                 160

Cys Tyr Glu Tyr Phe Ile Phe Asp Ile Phe Lys Tyr Ala Arg Asn Ile
                165                 170                 175

Leu Ser Leu Glu Val Asn Arg Gln Lys Glu Phe Tyr Pro Ile Lys Asn
            180                 185                 190

Lys Asn Asn Glu Tyr Gly Ile Leu Asn Ala Gln Lys Ala Leu Ser Asn
        195                 200                 205

Leu His Lys Ser Trp Leu Gln Tyr Lys Asn Ile Asn Ile Ile Asp Asn
    210                 215                 220

Lys Asp Glu Glu Lys Ile Phe Val Lys Tyr Leu Pro Leu Phe Leu Met
225                 230                 235                 240
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Met Glu His Ser Phe Leu Asn Cys His Lys Arg Gly Ile
245 250

<210> 17
<211> 984
<212> PRT
<213> Plasmodium falciparum

<400> 17

Met Glu Gly Phe Val Ala Leu Leu Ser Phe Leu Val Val Leu Val Phe
1 5 10 15

Asn Lys Thr Ile Gly Tyr Asn Ile Lys Ser Gly Asn Thr Ser Asn Asn
20 25 30

Ile Lys Tyr Val Asn Val Leu Asp Asn Asp Arg Asp Ile Asn Thr His
35 40 45

Ser Val Leu Pro Glu Val Glu Asn Val Ile Glu Arg Lys Asp Ile Tyr
50 55 60

Arg Gln Ile Asn Phe Met Glu Thr Phe Val Ser Ser Asn Asn Met Met
65 70 75 80

His Asp Arg Glu Lys His Thr Ser Asn Asp Ser Gly Ser Tyr Glu Ile
85 90 95

Thr Gly Ile Val Asp Gly Met Lys Ile Gly His Pro Ile Ser Val Ala
100 105 110

Leu Gly Ser Gln Tyr Ser Asn Tyr Phe Asp Tyr Leu Gln Ile Val His
115 120 125

Leu Asp Tyr Thr Asn Ser Arg Phe Ser Phe Thr Val Gly Glu Gly Lys
130 135 140

Tyr Tyr Leu Arg Thr Tyr Gly Ser Thr Tyr Met Thr Pro Ser Ala Ile
145 150 155 160

Lys Ile Lys Val Pro Cys Glu Lys Cys Lys Phe Ile Asn Ser Glu Tyr
165 170 175

Ser Gly Ile Ile Lys Ile Ile Pro Tyr Glu Thr Asn Asn Asn Leu Phe
180 185 190

Ile Tyr Asn Trp Val Leu Gln Thr Ser Ser Pro Leu Ala Leu Glu Asn
195 200 205

Ile Asn Thr Val Phe Ser Asp Glu Ala Asp Leu Ile His Gly Asn Ser
210 215 220

Leu Ser Glu Glu Phe Lys Ile Asp Ser Ser Ala Ala Ala Thr Ser Leu
225 230 235 240

Asn Thr Phe Tyr Gly Ile Val Leu His Gly Ile Trp Ser Ser Glu Tyr
245 250 255

Ala Glu Arg Leu Leu Thr Val Ile Ser Glu Phe Pro Asp Cys Val Lys
260 265 270

Met Ser Ala His Asp Lys Asn Ala Arg Ser Lys Gln Arg Lys Asn Gln
275 280 285

Lys Trp Ile Leu Val Asn Glu Asp Leu Gly Ser Phe Asp Met Lys Met
290 295 300

Glu Val Cys Glu Glu Val Asn Cys Asp Tyr Ser Ala Ile Ile His Val
305 310 315 320

Ser Lys His Ala Phe Glu Tyr Ser Lys Lys Leu Val His Asn Arg Gly
325 330 335

Arg Asn Gly Arg Tyr Tyr Ser Arg Arg Val Glu Lys Ile Leu Ile Arg
340 345 350

Ala Leu Leu Ser Leu Asp Phe Ser Leu Phe Ile Thr Tyr Phe Gln Gln
355 360 365

Lys His Gly Val Thr Leu Leu Asp Pro Gln Tyr Asp Tyr Glu Leu Ile
370 375 380

Thr Asn Met Ser Gly Tyr Ser Ser Asn Asn Tyr Gln Ser Trp Asn His
385 390 395 400

Asn Leu Glu Glu Leu Val Glu Leu Ala Thr Ser Trp Asp Glu Tyr Pro
405 410 415

Lys Gly Leu Gln Lys Val Gln Gly Leu Ser Tyr Leu Leu Arg Arg Lys
420 425 430

Asn Gly Thr Lys His Pro Val Tyr Pro Thr Ala Pro Ala Val Ala Phe
435 440 445

Pro Ala Gly Ser Gln Asn Asn Ser Phe Ile Glu Phe Met Glu Ser Ala
450 455 460

Phe Val Asn Tyr Val Asp Ile Ser His Leu Val Ile His Glu Val Ala
465 470 475 480

His Phe Ile Trp Val Asn Thr Val Ser Lys Glu Leu Lys Glu Lys Trp
485 490 495

Ile Gln Ile Gly Gln Trp Tyr Lys Glu Pro Leu Ser Pro Ser Glu Trp
500 505 510

Ala Thr Lys Leu Glu Val Glu Phe Val Ser Ala Tyr Ala His Asp Lys
515 520 525

Asn Pro Ala Glu Asp Phe Ala Glu Ser Met Ala Thr Tyr Val Leu Asn
530 535 540

Ser Lys Leu Leu Asn Ser Arg Ser Phe Asp Lys Phe Lys Trp Ile Gln
545 550 555 560

Asp Asn Leu Phe Gly Gly Gly Phe Tyr Ile Thr Thr Gly Thr His Lys
565 570 575

Phe Asp Val Ile Asn Leu Gly Asn Glu Val Tyr Tyr Phe Pro Gly Lys
580 585 590

Val Thr Arg Val Arg Ala Lys Val Leu Gly Ser Pro Thr Glu Asp Lys
595 600 605

Leu Val Lys Ile Tyr Ile Ser Leu Leu Ser Ser Asp Gly Ser Glu Gly
610 615 620

Cys Ala Lys His Gly Tyr Ala Arg Ile Phe Ser Glu Gln Gln Thr Phe
625 630 635 640

Arg Asp Leu Tyr Phe His Thr Glu Asp Arg Ser Pro Cys Ser His Lys
645 650 655

Leu Tyr Gly Glu Phe Thr Met Asn Lys His Glu Ser Arg Gly Arg Trp
660 665 670

Thr Ala Glu Ser Met Ile Phe Thr Gly Glu Asn Asn Ile Glu Arg Tyr
675 680 685

Val Gly Leu Gly Ser Phe His Phe Tyr Leu Tyr Val Asn Asn Gln Asn
690 695 700

Glu Asp Val Glu Lys Pro Ile Pro Leu Leu Asp Ser Ile Ser Ile Tyr
705 710 715 720

Thr His Asn Ala Thr Glu Thr Asn Asp Ala Leu Leu Arg Leu His Val
725 730 735

Met Val Leu Glu Asn Glu Leu Ile Lys Glu His Gly Gly Pro Tyr Ala
740 745 750

Ser Phe Ala Ala His Glu Asn Lys Ser Tyr Ser Tyr Glu Ser Arg Thr
755 760 765

Tyr Lys Met Tyr Pro Pro Glu Phe Asn Thr Leu Met Leu Lys Ala Asp
770 775 780

Tyr Phe Ile Arg Asp Ile Asn Thr Arg Gly Phe Arg Glu Val Asn Met
785 790 795 800

Asp Ser Cys Lys Ser Tyr Thr Asn Met Asp Thr Arg Asn Leu Lys Cys
805 810 815

Phe Gln Val Leu Asn Pro Val Thr Ile Pro Lys Tyr Cys Ile Gly Ser
820 825 830

Thr Tyr Phe Leu Arg Gln Val Ser Ile Glu Asp Ile Ala Gly Asn Leu
835 840 845

Glu Thr Val Asn Ile Ser Ser Asp Lys Tyr Ser Ala Arg Leu His Pro
850 855 860

Ile Gly Val Arg Asp Lys Gln Lys Pro Val Val Ser Asn Val Arg Val
865 870 875 880

Ser Ser Lys Pro Ala Asn Glu Tyr His Asp Gly Glu Thr Ile Val Ser
885 890 895

Leu Ser Phe Asn Val His Asp Asn Leu Ser Gly Val Tyr Tyr Ile Phe
900 905 910

Val Tyr Leu Arg Asp Pro His Gly Gly Lys His Arg Ser Asp Ile Asp
915 920 925

Arg Ala Ser Leu Pro Thr Gly Thr Glu Asn Lys Gln Ile Asn His Lys
930 935 940

Ile Leu Leu Pro Lys Gly Ser Met Gly Gly Thr Trp Met Leu Glu Glu
945 950 955 960

Ile Lys Ala Val Asp Ser Cys Lys Asn Glu Ser Arg Asn Ile Tyr Thr
965 970 975

His Ser Val Tyr Val Gln Asn Asp
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<210> 18
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<212> PRT
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<400> 18

Met Phe Tyr Ile Ile Tyr Phe Val Leu Ala Cys Val Leu Leu Ile Tyr
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Ile Arg Ile Arg Asn Lys Ala Thr Ser Thr Phe Phe Phe Phe Leu Ser
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Arg Phe Leu Leu Ile Cys Gly Phe Cys Ile Glu Leu Tyr Asp Asn Ile
35 40 45

Ser Asn Asp Ile Leu Asn Val Leu Ile Thr Tyr Ser Phe Thr Val Ser
50 55 60

Tyr Ile Phe Phe Met Ser Phe Lys Ile Leu Glu Ala Leu Leu Val Cys
65 70 75 80

Ile Ser Ile Leu Leu Leu Thr Phe Gly Val Tyr Tyr Glu Lys Asn Lys
85 90 95

Asn Met Ile Asp Ile Cys Thr His Phe Cys Ser Asn Pro Tyr Leu Ser
100 105 110

Ile Asn Asn Leu Asp His Met Asn Ile Ser Cys Leu Cys Lys Lys Gln
115 120 125

Ile Val Ile Phe Leu Ile Ser Leu Leu Ser Phe Thr Leu Ile Cys Leu
130 135 140

Ser Met Lys Tyr Tyr Glu Ile Phe Tyr Leu Lys Lys Lys Phe Leu Phe

145 150 155 160

Arg Tyr Lys Gln Lys Val Asn Leu Ala Lys Gln Ile Glu Ile Leu His
165 170 175

Thr Met Leu Pro Asn Phe Leu Val Glu Tyr Leu Leu Ile Ser Asp Pro
180 185 190

Lys Asn Asp Gly Ile Met Val Gly Lys Asn Ile Ser Gly Glu Asp Arg
195 200 205

Gly Ile Ile Ser Val Ile Phe Cys Asp Ile Asp Asp Phe Gln Asn Met
210 215 220

Val Ser Thr Leu Gln Pro His Val Leu Val Glu Thr Leu Asp Asn Leu
225 230 235 240

Tyr Leu Tyr Phe Asp Lys Cys Ile Lys Tyr Phe Asn Cys Ile Lys Ile
245 250 255

Glu Thr Val Phe Glu Ser Tyr Leu Ala Ala Ser Gly Leu Ser Glu Lys
260 265 270

Lys Asn Asn Ala Leu Asp Lys Ile Met Tyr Asp Thr Lys Cys Ala Ile
275 280 285

Lys Leu Ala Ile Ala Gln Leu Ser Ala Lys Tyr Tyr Ile Ser Tyr Lys
290 295 300

Val Leu Asp Thr Arg Glu His Phe Ser Asp Asn Ser Thr Ser Tyr Asp
305 310 315 320

Lys Tyr Ile Asn Lys Asn Ile Ser Leu Lys Ile Gly Ile His Thr Gly
325 330 335

Lys Ala Ile Ser Gly Val Ile Gly Ser Val Lys Pro Gln Tyr Ala Leu
340 345 350

Phe Gly Asp Thr Val Asn Thr Ala Ser Arg Met Lys Ser Thr Ser Leu
355 360 365

Pro Asp His Ile His Val Ser Tyr Asp Thr Tyr Lys Tyr Leu Lys Glu
370 375 380

Asp Asn Thr Phe Ile Trp Lys Glu Arg Lys Val Phe Ile Lys Gly Lys
385 390 395 400

Gly Lys Met Lys Thr Tyr Leu Leu Val Asp Ile Leu Asp Asp Val Lys
405 410 415

Arg Lys Gly Glu Ser Leu Asn Tyr Tyr Ser Ser Ser Asn Leu Leu Leu
420 425 430

Ser Gln Leu Gly Ser Glu Ala Val Ser Ile Tyr Glu Glu Arg Glu Asp
435 440 445

Ile Lys Glu Gly Ser Met Asp Ile Ile Lys Glu Ser Ser Arg Asp Ile
450 455 460

Ile Lys Glu Asp Ser Arg Asp Ile Ile Lys Glu Ile Ser Thr Asn Ile
465 470 475 480

Ser Lys Ser Ser Ser Arg Asn Ile Ser Lys Ser Ser Ser Arg Ser Ile
485 490 495

Ser Asp Ile Lys Glu Gly Gln Ile Ile Asp Lys Glu Asp Leu Ile Phe
500 505 510

Lys Ile Asn Arg Met Lys Asn Lys Ile Asp Ser Arg Tyr Ser Lys Arg
515 520 525

Ile Asp Lys Glu Ser Arg Asp Lys Ile Ser Asp Lys Thr Asn His Val
530 535 540

Leu Asp Glu Val Val Lys His Ser Asp Ile His Leu Leu Asn Tyr Glu
545 550 555 560

Ile Asn Asn Lys Arg Cys Lys Lys Met Lys Gly Asp Thr Asn Asn Glu
565 570 575

Asn Lys Leu Ile Gly Asp Ile Phe Asn Met Tyr Asp Lys Lys Ile Lys
580 585 590

Tyr Ile Tyr Lys Lys Asn Tyr Lys Ser Lys Ser Met Glu Asn Ile Ser
595 600 605

Phe Ile Lys His Tyr Arg Asn Thr Lys Tyr Lys Lys Ser Asp Tyr Leu
610 615 620

Leu Leu Asp Asn Lys Gly Glu Ser Lys Lys Phe Lys Arg Asn Thr Ser
625 630 635 640

Tyr Val Leu Glu Ser Pro Leu His Leu Ile Gly Asp Ile Val Asp Asn
645 650 655

Asn Ile Lys Arg Lys Lys Lys Lys Glu Ile Lys Thr Ile Val Ser
660 665 670

Asp Asp Met Phe Thr Ser Pro Val Asn Ile Lys Glu Tyr Asn Tyr Asn
675 680 685

Glu Gln Glu Arg Lys Lys Glu Ile Val Gly Asn Leu Ser Tyr Asp Lys
690 695 700

Thr Lys Lys Ile Phe Pro Phe Ile Lys Phe Thr Lys Glu Gly Arg Ile
705 710 715 720

Lys Lys Lys Lys Ile Glu Lys Lys Glu Lys Lys Glu Lys Lys Glu Asn
725 730 735

Asn Asn Asn Phe Leu Tyr Asn Asp Asp Tyr Ser Ser Tyr Ser Ser Pro
740 745 750

Lys Tyr Gly Asp Asn Glu Asn Asn Phe Val Ile Lys Tyr Ile Arg Glu
755 760 765

Arg Lys Asp Phe Gln Lys Lys Phe Asp His Pro Asn Phe Asn Phe Ser
770 775 780

Lys Phe Leu His Asn Tyr Asn Pro Met Lys Asn Lys Asn Lys Asn Lys
785 790 795 800

Lys Asn Asn Lys Asn Val Arg Arg Asn Glu Tyr Pro Asn Tyr Thr Ser
805 810 815

Ser Ser Lys Asp Gly Val Ser Tyr Asn Phe Leu Ser Asp Ser Leu Phe
820 825 830

Ser Ser Asp Asn Glu Tyr Ser Ser Asp Asn Glu Tyr Ser Ser Asp Ser
835 840 845

Glu Lys Tyr Tyr Lys Lys Arg Phe Lys Lys Asn Lys Lys Ile Ile Lys
850 855 860

Phe Asp Asp Leu Phe Thr Lys Ile Tyr Ile Lys Lys Lys Arg Leu Leu
865 870 875 880

Gln Met Asn Asn Tyr Asp Val Lys Gly Lys Gly Lys Lys Leu Lys Asn
885 890 895

Lys Gly Met Glu Arg Asn Lys Thr Lys Tyr Lys Asn Val Asn Glu Ile
900 905 910

Thr Lys Met Lys Tyr Phe Val Asn Asn Glu Asn Arg Asp His Glu Val
915 920 925

Asn Lys Glu Asp Ile Ser Lys Ser Met Gln Lys Tyr Phe Leu His Ile
930 935 940

Ser Lys His Lys Lys Glu Gln Ile Glu Asp Lys Lys Lys Thr His Lys
945 950 955 960

Tyr Phe His Lys Asn Val Glu Cys Val Tyr Pro Tyr Ala Gly Asn Asn
965 970 975

Ile Asn His Asn Phe Ser Arg Asn Glu Lys Arg Lys Tyr Ser Ile Asn
980 985 990

Leu Tyr Asp His Leu Asp Glu Gln Glu Lys Ile Lys Gly Lys Lys Lys
995 1000 1005

Tyr Phe Asn Lys Asp Lys Glu Leu Ile Gly Ser Ile Asn Lys Gln
1010 1015 1020

Thr Glu Arg Lys Pro Lys Lys Lys Asn Lys Lys Asn Ile Glu Asn
1025 1030 1035

Lys Lys Asp Lys Lys Lys Ile Arg Met Ile Thr Asn Lys Thr Lys
1040 1045 1050

Glu Lys His Ser Asn Ser Ile Ile Ser Val Glu Glu Gln Asn Met
1055 1060 1065

Asn His Asn Asn Ser Leu Lys Lys Lys Glu Val Asn Phe Thr Gly
1070 1075 1080

Lys Asn Glu Glu Tyr Leu Asn Arg Ala Asn Thr Asn Cys Ser Leu
1085 1090 1095

Gly Ile Lys Glu Met Glu Glu Asp Val Tyr Glu Phe His Ser Asn
1100 1105 1110

Asn Ile Tyr Tyr Asn Asn Gln Thr Ser Tyr Ser Asp Asp Ile Asn

1115 1120 1125

Asn Thr Thr Lys Leu Lys Gly Met Gly Asn Asn Thr Asn Asp Ile
1130 1135 1140

Ser Lys Asn Lys Gly Lys Asn Lys Leu Gly Lys Lys Ile Ser Phe
1145 1150 1155

Phe Ser Met Asn Asn Lys Tyr His Glu Ser Glu Ile Met Asn Glu
1160 1165 1170

Glu Asp Asn Lys Asn Met Leu Asn Leu Thr Gln Ser Gln Ile Ile
1175 1180 1185

Asn Lys Asp Lys Tyr Asn Tyr Phe Thr His Cys Pro Ser Leu Lys
1190 1195 1200

Lys Lys Lys Ser Val Phe Thr Lys Ile Asn Asn Leu Phe Lys Asn
1205 1210 1215

Tyr Phe Lys Ser Ile Asp Val His Glu Lys Phe Gly Phe Ser Lys
1220 1225 1230

Lys Phe Lys Phe His Ser Lys Asp Ser Asp Asp Ile Lys Gly Asn
1235 1240 1245

Asn Asn Lys Ile Ser Lys Asn Arg Tyr Asn Asn Asn Asn Asn Asn
1250 1255 1260

Asn Asn Ser Asn Tyr Ser Asn Ile Asp Ser Gly Lys Tyr Ser His
1265 1270 1275

Asn Asn Lys Lys Asn His His His Asn Asn Asn Lys Tyr His His
1280 1285 1290

His Asn Asn Asn Lys Tyr His His His Asn Asn Asn Lys Tyr His
1295 1300 1305

His Gln Asn Asn Asn Tyr Glu Lys His His His Ser Asn Asn Ser
1310 1315 1320

Arg Val Met Leu Ser Lys Gly Glu Lys Thr Glu Lys Asn Glu Asn
1325 1330 1335

Val Asp Tyr Ala Tyr Gln Phe Asp Asn Tyr Asp Lys Lys Leu Leu
1340 1345 1350

Lys Lys Leu Thr Ser Asn Leu Gln Leu Asn Lys Lys Asn Val Lys
1355 1360 1365

Asn Phe Asn Met Phe Tyr Tyr Lys Phe Asn Asp Glu Glu Leu Glu
1370 1375 1380

Glu Glu Tyr Thr Arg Asn Tyr Tyr Arg Glu Ile Ile Asn Ile Asp
1385 1390 1395

Leu Thr Lys Lys Leu Ile Ile Ile Phe Ile Phe Thr Glu Ile Phe
1400 1405 1410

Leu Ser Leu Cys Asn Ile Ile Glu Leu Ser Phe Tyr Glu Lys Lys
1415 1420 1425

Leu Arg Tyr Asn Asp Ser Ile Val Ile Ile Trp Leu Ile Arg Ser
1430 1435 1440

Ile Tyr Leu Phe Ile Ile Thr Tyr Ile Trp Ile Ile Leu Lys Thr
1445 1450 1455

Lys Leu Lys Glu Tyr Lys Asn Asn Ser Ser Lys Met Met Trp Thr
1460 1465 1470

Ile Phe Ile Leu Asn Ile Phe Leu Cys Ser Trp Gly Ile Ile Leu
1475 1480 1485

Ile Asp Leu Ser Cys Ile His Tyr Ser Met Leu Leu Gly Asn Lys
1490 1495 1500

Asn Glu Arg Ala Leu Phe Phe Met Lys Asp Ala Ser Glu Leu Ile
1505 1510 1515

Ile Cys Ile Gln Leu Ile Phe Ile Lys Asn Met Leu Phe Lys His
1520 1525 1530

Lys Phe Phe Phe Phe Val Phe Phe Tyr Ile Phe Leu Ile Tyr Ser
1535 1540 1545

Phe Ser Lys Leu Phe Ser Ile His Thr Cys Gln Thr His Ile Cys
1550 1555 1560

Cys Ser Ile Ile Leu Phe Ile Ser Ile Asn Ile Leu Tyr Phe Trp
1565 1570 1575

Tyr Ser Glu Tyr Leu Asp Arg Ile Gln Phe Leu Val Lys Arg Lys
1580 1585 1590

Arg Asn Arg Met Glu Lys Ile Ser Gln Asp Phe Leu Thr Lys Ile
1595 1600 1605

Leu Pro Arg Gln Val Leu Glu Glu Tyr Gln Asn Asp Asn Leu Gln
1610 1615 1620

Leu Thr Tyr Lys His Glu Lys Ile Ala Phe Leu Phe Ala Asp Ile
1625 1630 1635

Val Gly Phe Thr Lys Trp Ser Lys Thr Val Ser Pro Lys Glu Val
1640 1645 1650

Leu Lys Leu Leu Gln Lys Leu Ile Ser Lys Ile Asp Lys Asp Thr
1655 1660 1665

Ile Lys Leu Gly Leu Tyr Lys Leu Phe Thr Ile Gly Asp Ala Tyr
1670 1675 1680

Val Ala Thr Ser Gln Pro Asn Ser Ser Ile Thr Asp Glu Ser Glu
1685 1690 1695

Ala Leu Glu Gly Ile Leu Asn Ile Leu Lys Leu Ala Lys Leu Ile
1700 1705 1710

Leu His Asn Ile Asn Thr Ile Lys Ile Gln Phe Asn Lys His Asp
1715 1720 1725

Phe Asn Met Arg Ile Gly Leu His Tyr Gly Ser Cys Val Gly Gly
1730 1735 1740

Ile Ile Gly Ser Val Arg Ile Arg Tyr Asp Met Trp Gly Leu Asp
1745 1750 1755

Val Leu Ile Ala Asn Lys Ile Glu Ser Asn Gly Ile Pro Gly Glu
1760 1765 1770

Ile Ile Cys Ser Glu Gln Phe Arg His Phe Phe Ile Gln Asn Glu
1775 1780 1785

Pro Gln Ala
1790

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<400> 19

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Tyr Thr Phe Cys Phe Leu Pro Val Leu Gln Thr Gln Leu Gly Lys Ile
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Ile Asn Lys Val Ile Ser Ser Lys Tyr Phe Phe Lys Asn Asp Asp Ile
35 40 45

Cys Tyr Asn Lys Asn Asn Leu Asp Phe Lys Trp Tyr Leu Lys Lys Asp
50 55 60

Arg Lys Lys Ser Arg Lys Ile Lys Lys Lys Gln Lys Lys Arg Lys Arg
65 70 75 80

Lys Met Ile Met Met Lys Arg Gly Val Glu Asn Val Lys Asn Ala Asp
85 90 95

Ser Ser Asn Asn Asp Val Cys His Asp Gln Asn Asn Asn Asn Phe Asn
100 105 110

Asp Pro Leu Val Ser Lys Asn Thr Asn Tyr Asn Tyr Leu Tyr Thr Asn
115 120 125

Asn Asn Glu Asn Asn Met Lys Glu Ser Thr Phe Leu Lys Ile Asp Glu
130 135 140

Ser Tyr Leu Ser Thr Ser Tyr Ile Leu Asn Gly Lys Phe Val Ser Gly
145 150 155 160

Asn Asn Ile Ser Asp Asn Lys Asn Asp Leu Asn Glu Lys Lys Tyr Ile
165 170 175

Asn Ile Lys Arg Thr Asn Ser His Asn Asp Thr Ser Ser Leu Ser Ile
180 185 190

Ser Gln Asn Asn Phe Ser Lys Ile Lys Lys Lys Lys Gly Ala Ser Ser
195 200 205

Ile Asn Ser Tyr Asp Glu Ser Ser Pro Asn Val Ser Pro Pro Ser Met
210 215 220

Tyr Ser Ser Glu Asn Leu Ser Tyr Asn Glu Lys Arg His Asn Asn Asn
225 230 235 240

Ser Asp Asn Asn Asn Asp Arg Asn Met Lys Ser Tyr Asn Tyr Ser Ser
245 250 255

Ser Asn Ile Asn Lys Asn Cys Ser Ser Ser Ser Thr Ser Ser Ser Ile
260 265 270

Ser Ser Ser Ser Ile Ser Ser Ser Ser Ile Ile Ser Ser Ser Ile Ile
275 280 285

Ser Ser Ser Cys Ser Ser Val Thr Cys Ser Asp Ser Ser Leu Asn Ile
290 295 300

Tyr Asn Thr Lys Arg Ser Ser His Gly Ser His Asn Gln Phe Cys Gly
305 310 315 320

Ser Met Ser Cys Tyr Glu Lys Asp Lys Lys Lys Asn Arg Leu Asp Asn
325 330 335

Lys Asn Lys Met Lys Asn Lys Asn Ile Leu Asn Lys Lys Lys Lys Tyr
340 345 350

Lys Asn Lys Lys Met Pro Lys Thr Ile Asp Gly Asn Asp Thr Ser Leu
355 360 365

Leu Leu Ser Ser Ser Thr Ser Ser Cys Asn Thr Lys Val Ser Phe Asp
370 375 380

Asn Asn Glu Asn Tyr Gly Ile Ile Lys Glu Phe Ser Leu Cys Lys Ile
385 390 395 400

Asn Leu Phe Ile Lys Glu Ala Lys Leu Leu Phe Phe Asn Lys Asn Ile
405 410 415

Ser Ile Ser Asp Val Ser Leu Tyr Val Thr Thr Ile Met Glu Asp Lys
420 425 430

Lys Tyr Ile Gly Lys Leu Arg Lys Leu Ser Ser Arg Thr Leu Pro Met
435 440 445

Asn Asn Leu Ile Ile Asn Glu Tyr Ile Asn His Asn Ile Lys Asp Val
450 455 460

Tyr Thr Asp Ile Ile Ile Asn Ile Arg Tyr Lys Asn Arg Lys Lys Glu
465 470 475 480

Lys Glu Asp Ile Ile Leu Gly Arg Ala Ile Ile Pro Leu Phe Leu Ile
485 490 495

Leu Asn Thr Tyr Lys Trp Lys Ile Lys Lys Ile Lys Asn Lys Ile Arg
500 505 510

Tyr Cys Thr Lys Cys Phe Leu Trp Leu His Ile Phe Pro Cys Asn Asn
515 520 525

Lys Leu Phe Asn Tyr Lys Phe Phe Lys Pro Val Glu Gly Phe Glu Glu
530 535 540

Tyr Gly Met Leu Asn Pro Leu Tyr Thr Leu Gly Phe Leu Asn Ile Gln
545 550 555 560

Ile Lys Ile Ile Phe Lys Arg Asn Pro Leu Phe Leu Thr Phe Leu Ser
565 570 575

Asn Ile Arg Lys Pro Leu Phe Tyr Tyr Lys Leu Pro Val Gln Phe Glu
580 585 590

Pro Leu Tyr Cys Gln Tyr Tyr Ser Glu Asn Leu Tyr Val Tyr Ala Lys
595 600 605

Asn Ile Pro Leu Trp Ile Tyr Lys Phe Phe Tyr Ile Phe His Tyr Lys
610 615 620

Arg Leu Glu Met Ile Ser Leu Asn Cys Tyr Asp Tyr Ile Cys Ile Leu
625 630 635 640

Ile Phe Trp Leu Phe Phe Phe Asp Leu Val Val Leu Ser Pro Phe Ser
645 650 655

Leu Ile Phe Val His Leu Phe Phe Cys Ile Phe Phe Ile Ser Leu Ser
660 665 670

Tyr Lys Tyr Gly Lys Phe Val Pro Pro Tyr Tyr Lys Lys Lys Asn Leu
675 680 685

Phe Tyr Asn Phe Arg Pro Ile Arg Val Ser Arg Val Ser Arg Arg Asn
690 695 700

Cys Asp Tyr Thr Lys Arg Arg Ile Glu Thr Thr Asn Phe Ile Leu Asn
705 710 715 720

Asp Gln Lys Asn Val Glu Ile Tyr Asn Arg Glu Lys Lys Leu Asp Leu
725 730 735

Leu Asp Asp Asn Asn Val Asp Ala Asn Tyr Cys Lys Tyr Pro Tyr Cys
740 745 750

Ser Glu Glu Asn Asn Met Asp Lys Leu Asn Lys Asp Gly Arg Asp Val
755 760 765

Asn Lys Gly Val Asp Lys Asn Ile Ile Lys Gly Lys Asn Met Met Thr
770 775 780

Arg Gly Gly Gly Leu Asn Ile Tyr Asp Ala Cys Lys Met Phe Ile Lys
785 790 795 800

Gly Asp Thr Val Met Lys Ala Asn Ile Ile Asn Asp Asn Ile Val Tyr
805 810 815

Glu Asn Phe Ile Lys Asp Gly Ile Lys Lys Asn Asp Val Met Met Asp
820 825 830

Ser Glu Glu Asp Lys Glu Ile Asn Ala Val Tyr Ile Asn Asn Lys Asn
835 840 845

Val Tyr Asn Asn Asn Asn Ala Pro Val Ser Cys His Asp Cys Asp Asp
850 855 860

Pro Asn Asn Leu Ser Val His Val His Lys Glu Glu Asn Asn Ser Thr
865 870 875 880

Ser Asn Lys Met Ile Leu Pro Ser Val Cys Ser Glu Asn Ser Leu Lys
885 890 895

Glu Thr Met Gly Asn Gln Ser Met Glu Asn Asn Asn Lys Ile Asn Asn
900 905 910

Glu Asn Asn Asn Asp Val Asp Ser Val Glu Lys Thr Asp Ile Leu Leu
915 920 925

Asn Leu Ser Asn Gly Lys Asn Asn Gly Asn Val Thr Ser Ser Leu Cys
930 935 940

Glu Asn Leu Phe Val Tyr Asn Gln Asp Lys Ile Gln Arg Lys Lys Lys
945 950 955 960

Val Pro Tyr Lys Asn Lys Glu Arg Asp Asn Lys Asp Asp Leu Asp Glu
965 970 975

Lys Lys Asp Met Tyr Ile Cys Asn Asp Asp Ser Ser Val Ile Thr Ser
980 985 990

Ser Glu Lys Gly Val Thr Lys Glu Arg Ile His Met Asn Lys Glu Lys
995 1000 1005

Leu Asn Tyr Asn Gly Ser Met Glu Cys Ser Ser Val Cys Val Glu
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Lys Asn Asn Met Ser Tyr Ile Ala Arg Arg Ile Gln Asn Met Met
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Tyr Asp Thr Lys Glu Lys Met Lys Leu Asp Gln Ile His Met Asn
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Lys His Met Ser Gly Phe Met Lys Leu Phe Asn Val Lys His Val
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Glu Asn Glu Lys Glu Asn Asp Ile Asp Lys Tyr His Asp Lys Gly
1070 1075 1080

Glu Ser Asp Lys Gln Val Pro Ser Ser Val Gly Ser Tyr Lys Leu
1085 1090 1095

Met Ile Ser Gln Glu Ala Glu Phe Glu Glu Glu Glu Phe Asp Glu
1100 1105 1110

Lys Glu Glu Phe Asp Glu Lys Glu Glu Phe Asp Glu Glu Glu Glu
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Glu Gly Gly Gln Asp Glu Glu Ser Lys Lys Met Ser Arg Val Lys
1130 1135 1140

His Ile Lys Lys Arg Glu Asn Ile Ile Asn Ile Glu Gly Glu Asn
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Ile Leu Ser Ser Asp Gly Lys Lys Ser Glu Tyr Ile Ile Lys Asp
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Ser Met Asn Asn Thr Glu Tyr Ile Asn Asp Ile Ile Tyr Tyr Asn
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Asn Cys Asp Asn Ile Leu Glu Asp Asn Lys Ser Glu Tyr Asn Thr
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Ser Met Asn Glu Arg Val Met Asp Asn Lys Gln Glu Val Asn Lys
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Arg Ser Asn Asn Phe Phe Phe Ser Tyr Asn Asn Asn Asn Asn Asn
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Asn Asn Ile Asn Asn Asn Asn Asn Asn Lys Asn Glu Ser Val Trp
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Arg Asn Leu Leu Gly Ile Pro Ser Ser Asn Ile Glu Thr Val Asn
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Leu Asn Ser Asn Asn Cys Thr Glu Ile Lys Asn Ser Asn Lys Lys
1265 1270 1275

Phe Asn Ile Ile Asp Thr Tyr Gly Asn Asn Thr Leu Gln Asp Lys
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Ser Asn Ile Ile Asp Leu Arg Lys Lys Tyr Pro Tyr Met Pro Phe
1295 1300 1305

Val Lys Ser Pro Phe His Asn Phe Tyr Leu Tyr Met Asn Thr Asn
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Asp Asn Lys Asn Ile Ser Ile Phe Ser Asn Asn Val Glu Val Pro
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Asn Val His Val Ile Leu Asn Arg Phe Ile Thr Leu Ile Thr Trp
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Thr Gln His Val Ser Gly Ile Phe Thr Met Val Tyr Glu Lys Ile
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Lys Tyr Ala Phe Asn Trp Glu Phe Ser Phe Tyr Thr Leu Val Asn
1370 1375 1380

Ile Leu Ile Leu Phe Leu Ile Cys Tyr Ser Ile Ser Phe Ile Ile
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Tyr Met Phe Ser Tyr Ile Pro Phe Val Phe Phe Arg Phe Leu Phe
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Phe Val Thr Cys Ser Tyr Phe Ile Ile Arg Ser Tyr Glu Leu Thr
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Glu Asp Gly Asn Arg Ala Cys Leu Tyr Tyr Lys Lys Arg Lys Ile
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Gln Phe Leu Lys Asn Arg Lys Ile Ser Leu Ala His Gly Leu Phe
1445 1450 1455

Glu Thr Tyr Lys Trp Lys Asn Ile Ile Lys Ile Ile Lys Lys Thr
1460 1465 1470

Leu Lys Lys Lys Asp Thr Asn Ile Phe Lys Tyr Ile Cys Leu Thr
1475 1480 1485

Cys Ala Phe Lys Ile Tyr Lys Leu Phe Lys Ile Ile Phe Glu Asn
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Ile Leu Leu Tyr Ile Leu Phe Ile Leu Phe Phe Ile Lys Asn Trp
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Tyr Thr Arg Leu Leu Ile Leu Lys Asp Ile Glu His Met Gln Ile
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Ala Lys Leu Gln Gly Phe Lys Asn Leu Tyr Phe Phe Ile His Asn
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Arg Ile Ile Lys Arg Glu Gln Lys Asn Val Met Ser Asn Thr Ser
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Ser Asn Glu Ile Asn Asn Arg Lys Ser Ser Val Ile Lys Ile Val
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Asn Ile Asp Asp Met Glu Lys Asn Glu Glu Asn Met Asn Lys Asn
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Asp Asn Asn His Asp Lys Asn Asp Asp Ile Val Asp Val Asn Asn
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Val His Met Asn Ile Asn Asn Asp Asn Met Asn Thr Asn Asn Glu
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Tyr Glu Ile Ile Lys Arg Arg Asn Gln Asn Asn Met Leu Asp Gly
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Lys Arg Lys Ser Val Lys Ser Leu Met Tyr Glu Asn Tyr Lys Asn
1640 1645 1650

Leu Glu Ser Tyr Val Tyr Ser Ser Ser Asp Lys Glu Ala Val Ser
1655 1660 1665

Ile Ile Asn Glu Asp Asp Ile Ile Asp Glu Glu Glu Glu Glu Gly
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Asn His Gln Lys Glu Lys Leu Asn Lys Asp Asn Ile Asn Leu Asp
1685 1690 1695

Lys Lys Asn Ile Asn Thr Tyr Gln Asp Ile His Ile Asp Gln Glu
1700 1705 1710

Ile Gln Pro Cys Asp Asp Glu Asn Asp Asp Lys Leu Ser Leu Ser
1715 1720 1725

Gln Val Thr Asp Asn Gly Ala Met Asn Val Asn Val Asp Ile Phe
1730 1735 1740

Leu His Tyr Tyr Phe Lys Lys Arg Lys Tyr Asp Leu Phe Asn Asn
1745 1750 1755

Phe Ile Asn Ile Asn Arg Asn His Met Tyr Thr Tyr Lys Asp Ile
1760 1765 1770

Asn Leu Phe Tyr Ser Asn Glu Asp Gln Lys Met Asn Asn Ile Asn
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Tyr Gly Glu Tyr Leu Asn Ser Asp Asp Ala Tyr Ser Ser Ser Tyr
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Asp Tyr Asn Lys Arg Gln Lys Lys Lys His Val Lys
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<212> PRT
<213> Plasmodium falciparum

<400> 20

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Phe Thr Glu Asn Glu Asp Asp Leu Glu Asn Val Asn Met Lys Ser Ser
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Thr Lys Gly Ile Leu Asp Asp Asp Asn Ile Asp Asn Ser Asp Asp Asn
35 40 45

Asp Ser Asp Asn Asn Asn Gly Asp Asn Ser Asp Asp Asp Asp Asp Asp
50 55 60

Asp Asp Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Phe
65 70 75 80

Lys Lys Tyr Lys Glu Glu Glu Glu Lys Ile Lys Lys Phe Ile Glu Ile
85 90 95

Lys Lys Asp Ile Asn Asn Ile Glu Ser Cys Tyr Met Leu Asn Met Phe
100 105 110

Lys Phe Asn Leu Glu Ser Phe Lys Met Tyr Leu Ile Asn Ile Ile Glu
115 120 125

Asn Glu Ala Leu Glu Cys Ala Lys Asn Val Ile Glu Pro Leu Lys Lys
130 135 140

Lys Ser Asp Met Leu Ile Lys Lys Ile Asn Thr Leu Lys Ile Lys Leu
145 150 155 160

Lys Lys Lys Ile Ile Asp Ile Asp Ser Leu Tyr Tyr Val Ile Asn Ile
165 170 175

Ile Lys Lys Ile His Ile Phe Glu Ser Thr Ile Asp Ile Val Leu Asn
180 185 190

Pro Ile Asn Asp Met Leu Asn Ile Leu Glu Phe Tyr Met Ser Asn Phe
195 200 205

Leu Lys Lys Gln Met Asp Ser Leu Arg His Ser Asn Asn Tyr Asp Glu
210 215 220

Glu Glu Asn Tyr Gln Ile Lys Phe Ile Asn Asn Leu Glu Lys Lys Lys
225 230 235 240

Ser Ser Gly Gln Leu Tyr Asn Leu Asp Asp Ser Tyr Asn Lys Asn Leu
245 250 255

Leu Phe Thr Phe Asn Lys Leu Asn Val Met Lys Lys Lys Phe Val Ser
260 265 270

Phe Tyr Lys Phe Glu Val Glu Lys Lys Asn Leu Ile Leu Ser Lys Phe
275 280 285

Asn Glu Leu Ile Asn Leu Thr Lys His Val Glu Glu Glu Ile Gln Glu
290 295 300

Lys Lys Thr Thr Met Lys Asn Glu Leu Ile Asn Asn Ile Tyr Ser Phe
305 310 315 320

Lys Ile Asp Ile Lys Thr Phe Arg Glu His Phe Leu Lys Met Asn Phe
325 330 335

Lys Ser Glu His Ile Asn Pro Leu Asn Ala Phe Glu Leu Leu Lys Arg
340 345 350

Tyr Lys Glu Glu Ile Asn Met Leu Lys Asn Lys Tyr Asn Ser Tyr Tyr
355 360 365

Lys Gly Glu Ser Ile Phe Gly Leu Lys His Gln Thr His Ser Asp Leu
370 375 380

Phe Leu Ser Ser Asn Glu Ile His Asn Phe Tyr Ser Leu Tyr Asp Leu
385 390 395 400

Tyr Val Gln Leu Lys Glu Lys Leu Asn Glu Trp Lys Asn Leu Lys Trp
405 410 415

Phe Asp Gly Ile Gln Lys Met Lys Glu Leu Lys Asn Glu Ile Leu Ser
420 425 430

Phe Glu Lys Lys Cys Ser Gln Leu Pro Lys Asn Leu Lys Ile Ile Val
435 440 445

Ile Tyr Lys Asn Leu Met Lys Glu Ile Phe Tyr Phe Lys Glu Ile Thr
450 455 460

Pro Ile Val Asp Glu Leu Glu Lys Lys Asn Ile Leu Lys Arg His Trp
465 470 475 480

Ile Glu Ile Ile Asn Ile Leu Lys Glu Lys Lys Lys Lys Asp Ile Thr
485 490 495

Gly Lys Glu Lys Lys Ile Gln Lys Lys Ser Tyr Ala Asp Glu Gln Lys
500 505 510

Asp His Pro Lys Asp Asn Ile Asn Asn Lys Ser Asn Asn Asn Lys Asn
515 520 525

Asn Asn Lys Asn Asn Asn Ile Asn Asn Asn Asn Asn Gln Val Ile Asn
530 535 540

Glu Lys Val His Gln Ile Asp Pro Leu Val Asp Met Glu Lys Asn Asn
545 550 555 560

Val Leu Glu Asp Leu Asn Val Gln Gln Met Ser Asn Glu Asn Lys Asn
565 570 575

Val Lys Gln Val Glu Leu Ile Asn Asp Leu Glu His Gln Thr Asn Lys
580 585 590

Thr Ser Thr Gln Lys Asp Val Phe Glu Lys Asn Asp Asn Asn Asp Asn
595 600 605

Asn Asp Lys Asn Asn Ile Asn Leu Ile His Gly Asp Thr Asp Glu Asn
610 615 620

Met Tyr Asn Thr Ser Glu Phe Glu Asp Glu Lys Met Lys Lys Lys Asn
625 630 635 640

Ile Glu Asn Lys Lys Arg Ile Asn Asp Gln Thr Asp Glu Glu Ile Ile
645 650 655

Ser Lys Lys Asp Ile Ser Phe Gln Asp Gly Gly Leu Leu Glu Glu Ser
660 665 670

Ala Tyr Leu Asp Glu Glu Glu Tyr Ile Asn Asn Leu Asn Lys Leu Asp
675 680 685

Leu Asp Asn Met Asp Phe Phe Ile Lys Asp Ile Ile Asn Tyr His Leu
690 695 700

Leu Lys Lys Lys Asp Asp Ile Leu Asp Ile Cys Asp Ser Ala Glu Lys
705 710 715 720

Glu Ala Ser Ile Glu Glu Lys Ile Asn Glu Gln Tyr Lys Ile Trp Asn
725 730 735

Glu Thr Cys Phe Gln Phe Ser Lys Trp Lys Asn Arg Asp Tyr Ala Cys

740 745 750

Ile Leu Val Gly Ser Lys Val Ile Glu Ile Gln Glu Ser Leu Glu Glu
755 760 765

Ser Gln Ile Leu Leu Asn Asn Ile Asn Ser Thr Lys Tyr Ser Lys Pro
770 775 780

Phe Lys Ser Lys Leu Leu Leu Leu Leu Asn Lys Leu Ser Asp Cys Ser
785 790 795 800

Asp Ile Val Glu Arg Trp Ile Lys Val Gln Met Leu Trp Cys Ser Met
805 810 815

Glu Ser Val Phe Thr Ser Gly Asp Ile Ala Arg Gln Met Pro Ile Glu
820 825 830

Ser Lys Arg Phe His Gln Ile Asp Lys Asp Trp Ile Asn Ile Ile Asn
835 840 845

Ile Ala Asn Glu Ser Ser Ile Val Ile Glu Cys Cys Gln Ser Ser Met
850 855 860

Leu Lys Glu Leu Leu Pro Asn Met Gln Lys Gly Leu Glu Ser Cys Gln
865 870 875 880

Lys Ser Leu Glu Ser Tyr Leu Glu Gly Lys Arg Ser Lys Phe Pro Arg
885 890 895

Phe Tyr Phe Val Ser Asn Leu Val Leu Leu Lys Ile Leu Ser Gln Gly
900 905 910

Ser Asp Ile Asn Ile Ile Gln Ser Glu Leu Ile Lys Leu Phe Asp Ala
915 920 925

Ile Asn Tyr Leu Thr Ile Lys Thr Ile Gln Asn Lys Lys Arg Ile Ile
930 935 940

Cys Ile Asn Asn Lys Glu Lys Asp Asp Ile Glu Thr Val Gln Leu Val
945 950 955 960

Asn His Val Thr Ile Asp Gly Asn Ile Glu Asn Trp Leu Ile Leu Leu
965 970 975

Glu Lys Glu Met Gln Lys Ala Ile Lys Lys Glu Cys Lys Leu Gly Val
980 985 990

Ser Asn Ser Ser Gln Leu Phe Lys Thr Leu Asn Leu Lys Glu Phe Cys
995 1000 1005

Asp Lys Asn Ile Ala Gln Val Ala Leu Ile Cys Leu Gln Val Met
1010 1015 1020

Trp Thr Asn Asp Ile Glu Lys Cys Ile Tyr Lys Tyr His Ser Glu
1025 1030 1035

Lys Asn Ile Leu Lys Val Thr Asn Lys Lys Ile Asn Tyr Ile Met
1040 1045 1050

Ser Glu Leu Val Asn Ile Cys Leu Ser Asp Leu Gly Thr Lys Leu
1055 1060 1065

Asn Arg Thr Lys Tyr Glu Thr Leu Val Thr Ile His Val His Gln
1070 1075 1080

Arg Asp Leu Phe Thr Glu Ile Ser Ala Lys Ile Lys Glu His Lys
1085 1090 1095

Ile Lys Thr Thr Thr Asp Phe Asp Trp Ile Lys Gln Thr Arg Ile
1100 1105 1110

Tyr Tyr Lys Val Glu Lys Asn Ile Ile Leu Ile Ser Ile Ser Asp
1115 1120 1125

Val Asp Phe Ile Tyr Ser Tyr Glu Tyr Leu Gly Ile Lys Glu Arg
1130 1135 1140

Leu Cys Ile Thr Pro Leu Thr Asp Arg Cys Tyr Leu Thr Cys Ala
1145 1150 1155

Gln Ala Leu Gly Leu Cys Tyr Gly Gly Ala Pro Ala Gly Pro Ala
1160 1165 1170

Gly Thr Gly Lys Thr Glu Thr Val Lys Asp Leu Gly Arg Thr Leu
1175 1180 1185

Gly Ile Tyr Val Ile Val Thr Asn Cys Ser Asn Gln His Lys Tyr
1190 1195 1200

Lys Asp Met Ala Lys Ile Phe Lys Gly Leu Cys Arg Ser Gly Leu
1205 1210 1215

Trp Gly Cys Phe Asp Glu Phe Asn Arg Ile Asn Leu Asp Val Leu
1220 1225 1230

Ser Val Val Ala Met Gln Ile Glu Ser Ile Val Thr Ala Lys Lys
1235 1240 1245

Gln Ser Leu Lys Tyr Phe Leu Phe Pro Gly Asp Ser Lys Ser Ile
1250 1255 1260

Asn Leu Asn Pro Ser Ser Ala Tyr Phe Ile Thr Met Asn Pro Gly
1265 1270 1275

Tyr Ala Gly Arg Gln Leu Leu Pro Glu Asn Leu Lys Ile Phe Phe
1280 1285 1290

Arg Phe Ile Ser Met Met Val Pro Asp Arg Gln Ile Ile Ile Lys
1295 1300 1305

Val Lys Leu Ala Ser Val Gly Tyr Leu Asp Ile Asp Asn Leu Ser
1310 1315 1320

Asn Lys Phe Lys Ser Leu Tyr Asn Leu Cys Glu Glu Gln Leu Ser
1325 1330 1335

Lys Gln Lys His Tyr Asp Phe Gly Leu Arg Asn Ile Leu Ser Val
1340 1345 1350

Leu Arg Thr Ala Gly Asp Thr Lys Arg Ser Ala Gly Pro Asn Glu
1355 1360 1365

Asn Asp Glu Glu Met Leu Leu Met Arg Thr Leu Arg Asp Met Asn
1370 1375 1380

Leu Ser Lys Leu Ile His Asp Asp Val Leu Leu Phe Leu Ser Leu
1385 1390 1395

Leu Asn Asp Val Phe Pro Lys Phe His Asn Ile Thr Lys Lys Ser
1400 1405 1410

Phe Gln Leu Ile Glu Glu Asn Val Leu Gln Ile Ile Lys Lys Lys
1415 1420 1425

Lys Leu Cys Ala Lys Gly Lys Trp Ile Leu Lys Ile Leu Gln Leu
1430 1435 1440

Tyr Glu Thr Ser Leu Val Arg His Gly Phe Met Leu Val Gly Asn
1445 1450 1455

Thr Leu Thr Gly Lys Thr Glu Ile Leu Asn Ile Leu Thr Ser Ala
1460 1465 1470

Leu Thr Asn Ile Gly Ser Val Thr Lys Ile Ile Thr Leu Asn Pro
1475 1480 1485

Lys Ala Ile Thr Ser Glu His Met Tyr Gly Val Lys Asp Asn Leu
1490 1495 1500

Ser Glu Glu Trp Thr Pro Gly Ile Phe Ala Asn Ile Trp Glu Lys
1505 1510 1515

Tyr Asn Asn Asn Asn Leu Lys Tyr Asn Thr Trp Ile Val Cys Asp
1520 1525 1530

Gly Pro Val Asp Ala Ile Trp Ile Glu Asn Leu Asn Thr Val Leu
1535 1540 1545

Asp Asp Asn Lys Ile Leu Thr Leu Ala Asn Asn Asp Arg Ile Pro
1550 1555 1560

Met Thr Asp Asn Thr Lys Ile Ala Phe Glu Val Glu Asn Leu Asn
1565 1570 1575

Asn Ala Ser Pro Ala Thr Val Ser Arg Ala Gly Ile Val Tyr Ile
1580 1585 1590

Ser Asp Ser Asp Leu Gly Tyr Arg Pro Phe Ile Tyr Ser Trp Leu
1595 1600 1605

Gln Lys Leu Lys Asp Ile Asn Thr Tyr Gly Met Thr Leu Tyr Ala
1610 1615 1620

Ile Phe Asn Lys Leu Phe Ile Phe Tyr Leu Asp Lys Ile Gln Ile
1625 1630 1635

Leu Ser Phe Leu Lys Glu Asn Cys Lys Phe Val Met Asp Ile Thr
1640 1645 1650

Asp Ser Ile Leu Ile Leu Gln Thr Ile Asn Leu Leu Asn Ser Gln
1655 1660 1665

Ile Ile Gln Tyr Ile Asn Ala Ile Asn Asn Phe Met Tyr Asn Glu
1670 1675 1680

Glu Asp Leu Asn Lys Ile Phe Phe Leu Asp Thr Asn Glu Lys Lys
1685 1690 1695

Leu Leu Pro His Ser Gln Lys Leu Ile Lys Ser Asn Ile Glu Glu
1700 1705 1710

Glu Asn Asn Ile Tyr Glu Gln Glu Asn Gly Ile Pro Ser Ser Glu
1715 1720 1725

Met Lys Lys Gly Lys Asp Gln Leu Leu Asn Asp Glu Lys Tyr Lys
1730 1735 1740

Ser Ser Asn Lys Leu Glu Asp Thr Lys Asn Met Thr Leu Pro Asn
1745 1750 1755

Asp Leu Gly Lys Lys Pro Leu Phe Pro Thr Leu Glu Lys Lys Asn
1760 1765 1770

Asp Lys Tyr Gly Lys Asn Leu Asp Asn Ile Lys Asn Glu Gln Lys
1775 1780 1785

Asp Gln Asn Asp Glu Glu Lys Asn Lys Lys Met Asp Lys Lys Glu
1790 1795 1800

Ala Asp His Asp Gln Gln Gln Asp Glu Glu Glu Lys Glu Gln Glu
1805 1810 1815

Glu Glu Tyr Asp Asp Asp Thr Lys Leu Asp Gly Ile Asn Asn Tyr
1820 1825 1830

Thr Leu Ser Ser Gly Thr Lys Tyr Glu Lys Val Asn Ile Asp Glu
1835 1840 1845

Cys Glu Glu Ile Met Leu Tyr Ser Ile Val Trp Gly Leu Cys Gly
1850 1855 1860

Leu Leu Glu Tyr Lys Asp Arg Leu Lys Val His Asn Phe Leu Leu
1865 1870 1875

Lys Asn Val Pro Val Leu Lys Asn Val Met Gly Val Asn Lys Lys
1880 1885 1890

Leu Tyr Thr Glu Glu Asn Glu Lys Ile Lys Gln Gln Gln Pro Lys

1895 1900 1905

Lys Lys Lys Glu Leu Gln Pro Lys Gly Asp Tyr Asn Asp Tyr Val
1910 1915 1920

Ser Thr Lys Gln Asn Lys Glu Glu Asp Lys Asn Asn Ile Glu Leu
1925 1930 1935

Asp Asn Glu Gln Asn Val Glu Asp Gly Glu Glu Phe Glu Asn Glu
1940 1945 1950

Ile Ser Leu Ile Tyr Asp Phe Tyr Phe Asp Met Lys Leu Lys Lys
1955 1960 1965

Leu Val Lys Trp Asn Val Gly Pro Phe Lys Met Pro Arg Asn Ile
1970 1975 1980

Asn Ser Ile Ser Ser Ile Leu Ile Pro Thr Ile Glu Thr Thr Lys
1985 1990 1995

Val Glu His Ile Ile Lys Leu Ile Ser Asn Ile Pro Ile Arg Cys
2000 2005 2010

Tyr Asn Phe His Thr Tyr Lys Ser Thr Leu Leu Leu Gly Ser Thr
2015 2020 2025

Gly Ser Ala Lys Thr Ser Ile Ala Leu Leu Tyr Thr Ser Lys Gln
2030 2035 2040

Glu Lys Asn Thr Lys Arg Phe Asn Phe Ser Ser Val Thr Thr Pro
2045 2050 2055

Glu Lys Phe Gln Leu Phe Ile Glu Ser Glu Leu Glu Arg Lys Thr
2060 2065 2070

Gly Lys Thr Tyr Gly Pro Ile Gly Asn Thr Lys Ser Ile Ile Phe
2075 2080 2085

Ile Asp Asp Met Ser Met Pro Lys Ile Asn Glu Trp Gly Asp Gln
2090 2095 2100

Ser Thr Leu Glu Leu Leu Arg Gln Leu Ile Glu Phe Gln Gly Phe
2105 2110 2115

Tyr Phe Leu Asp Lys Asp Lys Arg Gly Asn Phe Lys Lys Ile Ile
2120 2125 2130

Asp Leu Glu Tyr Ile Gly Cys Ile Asn His Pro Gly Cys Gly Asn
2135 2140 2145

Asn Asp Ile Pro Lys Arg Leu Lys Ser Lys Trp Phe Asn Val Asn
2150 2155 2160

Ile Leu Pro Tyr Asn Leu Asn Ser Ile Asn Thr Ile Tyr Gly Thr
2165 2170 2175

Val Leu Arg Thr Lys Phe Asn Lys Lys Gln Asn Phe Ser Asp Glu
2180 2185 2190

Ile Ile Glu Asn Ile Asp Lys Val Ile Leu Cys Thr Ile Asn Leu
2195 2200 2205

Phe Gly Arg Leu Lys Lys His Leu Leu Pro Val Pro Ser Arg Phe
2210 2215 2220

His Tyr Leu Tyr Thr Thr Arg Asp Leu Ala Lys Ile Phe Tyr Ser
2225 2230 2235

Met Leu Leu Cys Pro Tyr Glu Ser Ile Asp Asn Asn Leu Tyr Asn
2240 2245 2250

Phe Leu Cys Leu Trp Lys His Glu Cys Glu Arg Val Leu Ile Asp
2255 2260 2265

Lys Leu Ser Arg Met Glu Asp Lys Thr Phe Ser Leu Asp Gln Leu
2270 2275 2280

Lys Gln Ile Phe Asn Gln Tyr Tyr Pro Ser Tyr Lys Asp Ile Cys
2285 2290 2295

Glu Lys Asn Ile Tyr Phe Ser Tyr Phe Tyr Val Ser Glu Lys Glu
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Gln Gln Leu Tyr Met Ile Glu Asn Asp Leu Ile Glu Asn Asn Thr
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Thr Gln Glu Lys Thr Glu Asn Asn Lys Ile Asn Ile Thr Ile Ser
2330 2335 2340

Pro Ser Tyr Ile Asn Asp Thr Ser Asn Asn Leu Ile Ser Thr Lys
2345 2350 2355

Leu Asp Asn Thr Asn Glu Leu Asn Glu Lys Ile Asp Asp Thr Lys
2360 2365 2370

Thr Arg Ser Asn Ser Ala Leu Tyr Arg Arg Asn Asp Val Asp Asn
2375 2380 2385

Gln Asn Ile Ile Asn Asn Asn Asn Ile Leu Thr Lys Glu Gly Asp
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Asn Asn Gly Asp Ile Asp Asn Ile Asn Thr Phe Ser Phe Ser Trp
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Met Lys Lys Asp Tyr Lys Ile Val Val Asp Phe Glu Arg Leu Arg
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Tyr Ile Val Tyr Glu Tyr Met Lys Glu Tyr Asn Ile Asn Asn Val
2435 2440 2445

Lys Lys Leu Asp Leu Val Phe Phe Asp Asp Ser Leu Lys His Leu
2450 2455 2460

Ile Ile Ile Asn Arg Val Met Gln Thr Pro Asn Gly Ser Cys Met
2465 2470 2475

Leu Val Gly Val Gly Gly Ser Gly Lys Arg Ser Leu Thr Lys Leu
2480 2485 2490

Ser Val Phe Ile Ser Glu Gln Val Leu Phe Gln Leu Asn Ile Thr
2495 2500 2505

Lys Thr Tyr Thr Lys Asn Leu Phe Phe Glu Asp Leu Lys Ser Leu
2510 2515 2520

Tyr Ile Ser Ala Gly Gln Met Asn Lys Lys Thr Thr Phe Leu Leu
2525 2530 2535

Ser Asp Ser Asp Ile Glu Lys Asn Asp Phe Ile Leu Glu His Val
2540 2545 2550

Asn Ser Ile Leu Ser Thr Gly Leu Val Tyr Gly Leu Phe Ile Lys
2555 2560 2565

Asp Glu Lys Glu Ala Ile Cys Ala Glu Met Lys Glu Ser Tyr Leu
2570 2575 2580

Lys Glu Met Asn Lys Ser Asn Gln Ser Ser Lys Ile Lys Gly Gly
2585 2590 2595

Lys Lys Lys Lys Asn Lys Asn Asp Tyr Asn Asn Ile Asp Asp Met
2600 2605 2610

Asp Met Asp Glu Phe His Ser Lys Asp Ser Gln Ser Lys Ser Asp
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Ala Ser Ser Thr Ser Ser Ile Asp Asn Asp Ser Ile Ser Asn Glu
2630 2635 2640

Asn Ile Thr Asn Lys Lys Lys Lys Lys Asp Glu Lys Val Ile Asn
2645 2650 2655

Asp Phe Asn Val Ser Ser Asn Val Ile Phe Asp Tyr Leu Leu Asp
2660 2665 2670

Asn Val Arg Asn Asn Leu His Ile Phe Leu Cys Phe Ser Pro Ile
2675 2680 2685

His Lys Glu Phe Ala Leu Arg Tyr Gln Gln Phe Pro Cys Ile Tyr
2690 2695 2700

Asn Cys Val Thr Ile Asn Trp Phe Leu Lys Trp Pro Leu Glu Ala
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Leu Val Asn Val Ser Thr Ala Tyr Leu Asn Asn Phe Asn Ile Asp
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Ile Glu Asp Asn Leu Lys Asp Asp Phe Phe Asn Leu Phe Ala Ile
2735 2740 2745

Val His Asn Lys Val Ser Asp Thr Cys Asp Thr Tyr Lys Glu Arg
2750 2755 2760

Met Arg Arg Asn Thr Tyr Val Thr Pro Lys Ser Tyr Leu Ser Phe
2765 2770 2775

Ile Asp Leu Tyr Lys Gln Met Tyr Val Lys Lys Tyr Asp Glu Ile
2780 2785 2790

Lys Cys Leu Lys Glu Ser Val Asp Ile Gly Leu Lys Lys Leu Asn
2795 2800 2805

Glu Ala Ala Met Asp Val Gln Lys Met Arg Glu Ser Leu Thr Ser

2810 2815 2820

Glu Glu Glu Lys Leu Lys Glu Ser Asp Glu Gln Met Asn Ile Leu
2825 2830 2835

Leu Glu Lys Val Lys Asp Glu Ser Leu Lys Ala Glu Lys Gln Ser
2840 2845 2850

Val Glu Val Ser Lys Phe Arg Asp Lys Cys Ile Lys Glu Lys Asp
2855 2860 2865

Leu Ile Leu Lys Asp Gln Glu Glu Ala Asp Lys Asp Leu Lys Ala
2870 2875 2880

Ala Leu Pro Tyr Leu His Glu Ala Glu Glu Ala Ile Lys Ser Ile
2885 2890 2895

Thr Gly Lys Asp Ile Thr Glu Leu Lys Ser Met Lys Thr Pro Ser
2900 2905 2910

Asp Ile Ile Arg Ile Val Phe Asp Gly Val Leu Ile Leu Leu Gln
2915 2920 2925

Gly Lys Leu Lys Glu Pro Lys Ile Asp Val Lys Tyr Val Asn Lys
2930 2935 2940

Gln His Ile Asp Phe Ile Gln Asp Ser Phe Asp Glu Tyr Ala Lys
2945 2950 2955

Pro Leu Met Ala Asp Ile Arg Phe Leu Asn Leu Leu Phe Asp Phe
2960 2965 2970

Ser Lys Asn Glu Lys Asp Asn Ile Asn Glu Glu Thr Ile Glu Leu
2975 2980 2985

Leu Lys Pro Tyr Ile Gln Ser Thr Phe Phe Lys Thr Gln Ile Ala
2990 2995 3000

Lys Lys Ala Ser Val Ala Ala Glu Gly Leu Cys Lys Trp Val Gly
3005 3010 3015

Ala Met Ala Met Tyr Asn Gln Ala Ser Lys Ile Val Lys Pro Lys
3020 3025 3030

Met Ser Tyr Leu Lys Ile Gln Thr Gly Arg Leu Glu Asp Ala Leu
3035 3040 3045

Lys Gln Leu Ala Glu Ala Glu Asp Ser Leu Leu Lys Ala Gln Leu
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Phe Val Glu Asn Leu Asn Leu Asp Ile Glu Asn Met Phe Lys Lys
3065 3070 3075

Lys Lys Ala Leu Glu Glu Thr Ala Leu Lys Thr Lys Gln Arg Ile
3080 3085 3090

Glu Gln Ala Asn Lys Leu Ile Asn Gly Leu Ser Ser Glu Lys Asp
3095 3100 3105

Arg Trp Thr Asp Asp Ser Asn Asn Phe Ser Asn Ile Lys Lys Lys
3110 3115 3120

Ile Val Gly Asp Val Phe Ile Cys Ser Ser Phe Ile Thr Tyr Cys
3125 3130 3135

Gly Met Phe Asn Thr Glu Phe Arg Asn Tyr Leu Met Asn Asp Val
3140 3145 3150

Phe Tyr Asn Tyr Thr Lys Asn Ile Lys Asn Ile Pro Val Ser Ser
3155 3160 3165

Asn Ile Asp Ile Ile Lys Tyr Val Leu Ser Ser Asp Asp Thr Lys
3170 3175 3180

Ile Cys Asp Trp Ser Val Gln Lys Leu Pro Asn Asp Lys Leu Ser
3185 3190 3195

Ile Glu Asn Ala Leu Ile Cys Glu Asn Ser Asn Lys Tyr Val Leu
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Leu Ile Asp Pro Gln Cys Gln Ala Ser Asn Trp Ile Lys Asn Lys
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Glu Phe Gln Asn Asp Leu Ser Asn Gln Arg Cys Ile Thr Thr Phe
3230 3235 3240

Asn Ser Thr Lys Phe Lys Asp Asn Leu Glu Tyr Cys Leu Ser Glu
3245 3250 3255

Gly Lys Thr Leu Leu Ile Glu Asn Val Glu Glu Tyr Ile Asp Pro
3260 3265 3270

Ile Leu Asp Ser Val Leu Glu Lys Gln Ile Ile Lys Lys Gly Lys
3275 3280 3285

Lys Asn Tyr Ile Leu Ile Glu Asn Asn Leu Ile Asn Phe Asp Glu
3290 3295 3300

Lys Phe Asn Leu Phe Met Thr Thr Asn Ile Pro Asn Pro Asn Tyr
3305 3310 3315

Ser Pro Glu Ile Tyr Ala Arg Cys Cys Val Ile Asp Phe Thr Val
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Thr Val Lys Gly Leu Glu Asp Gln Leu Leu Gly Arg Val Leu Thr
3335 3340 3345

Glu Glu Gln Lys His Leu Glu Ile Thr Leu Lys Asn Ile Met Ile
3350 3355 3360

Glu Leu Lys Asp Asn Thr Lys Ser Leu Gln Asp Leu Asp Lys Gln
3365 3370 3375

Leu Leu Tyr Lys Leu Asn Thr Ser Ser Ser Asn Leu Ile Glu Asp
3380 3385 3390

Glu Glu Leu Ile Glu Val Leu Asn Asn Thr Lys Leu Leu Ser Lys
3395 3400 3405

Glu Leu Glu Ser Lys Leu Lys Asp Ser Asn Glu Lys Lys Lys Glu
3410 3415 3420

Ile Asn Glu Lys Arg Glu Gln Tyr Arg Ser Val Ala Leu Arg Gly
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Ser Ile Leu Tyr Phe Cys Ile Val Asp Ile Thr Asn Val Asn Tyr
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Ile Tyr Asn Thr Ser Leu His Gln Phe Leu Glu Gln Phe Asp Leu
3455 3460 3465

Ser Ile Lys Lys Ala Glu Lys Gly Gln His Ile Lys Lys Arg Val
3470 3475 3480

Glu Ser Ile Leu Tyr Thr Leu Thr Asn Leu Ile Ile Ser Tyr Met
3485 3490 3495

Glu Arg Cys Leu Phe Asp His His Lys Ile Ile Phe Lys Leu Leu
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Ile Ser Leu Lys Ile Leu Leu Tyr Asp Asn Ile Ile Ser Asn Lys
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Asp Ile Ser Phe Phe Leu Asn Pro Leu Ser His Tyr Ser Pro Ser
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Asn Asp Met Asn Asn Glu Met Thr Asn Thr Asn Met Leu Asn Asp
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Pro Met Gly Val Leu Lys Asn Lys Lys Asn Lys Lys Asn Asn Lys
3560 3565 3570

Glu Met Ile Asn Asn Asn Asn Asn Met Ser Ile Ala Ile Asn Ala
3575 3580 3585

Val Ile Asn Asn Thr Met Asp Ser Ser Ser Met Asn Asn Asp Thr
3590 3595 3600

Met Asn Val Tyr Leu Gly Thr Asn Glu Asn Asp Lys Asn Lys Lys
3605 3610 3615

Asp Thr Asn Thr Ser Asp Val Met Ser Ser Ser Ser Ser Thr Lys
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Thr Gly Ser Arg Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr
3635 3640 3645

Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Met Asp Gly Asn
3650 3655 3660

Ser Ser Asn Asn Ala Gly Asp Ile Asn Ser Cys Lys Asn Asn Thr
3665 3670 3675

Ser Val Thr Asp His Asn Ile Ser Asn Lys Asn Lys Ile Asp Leu
3680 3685 3690

His Lys Lys Gly Ala Gly Lys Gly Lys Ile Ser Ser Thr Lys Trp
3695 3700 3705

Leu Phe Lys Asn Glu Lys Leu Tyr Lys Asn Ile Ile Ser Leu Ser
3710 3715 3720

Asn His Ser Phe Gly Asn Asp Lys Asn Asn Arg Phe Phe Tyr Asp
3725 3730 3735

Ile Leu Asn Val Ile Gln Leu Asn Glu Asn Thr Trp Lys Asn Tyr
3740 3745 3750

Tyr Asp Ile Leu Asp Ile Glu Asn Lys Asn Ile Pro Tyr Tyr Asn
3755 3760 3765

Glu Arg Leu Asp Val Asn Ser Gln Ile Ser Ser Phe Ile Lys Leu
3770 3775 3780

Cys Leu Ile Arg Cys Leu Arg Glu Asp Arg Thr Ile Leu Cys Ala
3785 3790 3795

Asn Lys Phe Val Asp Glu Val Leu Asn Arg Asn Ser Asp Thr Ile
3800 3805 3810

Lys His Glu Thr Leu Glu Asn Ile Phe Ser Glu Ser Ser Asn Arg
3815 3820 3825

Lys Pro Phe Leu Phe Leu Leu Ser Leu Ala Ser Asp Pro Thr Asn
3830 3835 3840

Met Ile Asp Asp Phe Ala Lys Lys Phe Lys Lys Tyr Pro Thr Asp
3845 3850 3855

Lys Ile Ser Met Gly Glu Gly Gln Glu Val Ile Ala Lys Glu Lys
3860 3865 3870

Leu Lys Asn Gly Ile Ile Ser Gly Asn Trp Leu Ile Leu Gln Asn
3875 3880 3885

Cys His Leu Asn Lys Asn Phe Ile Ile Asp Val Tyr Asn Met Leu
3890 3895 3900

Lys Asn Leu Asn Glu Ile Glu Glu Asp Phe Arg Leu Phe Leu Thr
3905 3910 3915

Ser Glu Pro Asp Asp Glu Phe Pro Ile Cys Ile Leu His Gly Ser
3920 3925 3930

Ile Lys Ile Ser Thr Ser Leu Ser Ser Gly Ile Lys Asn Asn Met
3935 3940 3945

Arg Lys Ile Tyr Lys Asp Ile Ile Lys Glu Asp Ile Leu Glu Lys

3950 3955 3960

Ile Asp Asp Asp Lys Tyr Arg Lys Ile Ile Tyr Ser Leu Ser Tyr
3965 3970 3975

Leu His Cys Val Leu Cys Glu Arg Lys Lys Phe Gly Pro Leu Gly
3980 3985 3990

Trp Cys Val Pro Tyr Glu Phe Ser Ile Thr Asp Leu Phe Ala Ser
3995 4000 4005

Tyr Leu Phe Ile Glu Lys His Leu Tyr Ser Thr Leu Leu Val Asn
4010 4015 4020

Arg Pro Ile Asp Trp Glu Ser Ile His Tyr Met Leu Ala Glu Val
4025 4030 4035

Gln Tyr Gly Gly Lys Val Thr Asp Asp Leu Asp Arg Glu Leu Leu
4040 4045 4050

Leu Thr Tyr Val Gln Tyr Tyr Phe Asn Glu Asp Leu Phe Arg Met
4055 4060 4065

Lys Ser Glu Gly Ser Ser Glu Tyr Leu Asn Leu Pro Lys Phe Tyr
4070 4075 4080

Glu Ile Thr Asn Phe Lys Asn Phe Ile Glu Lys Ile Pro Asn Ile
4085 4090 4095

Asp Thr Pro Ser Val Leu Asp Leu His Asn Asn Ala Glu Ile Thr
4100 4105 4110

Tyr Arg Val Asn Glu Ser Arg Gln Val Leu Asn Ser Ile Leu Glu
4115 4120 4125

Ile Gln Pro Arg Asp Val Asp Gln Gly Glu Glu Lys Ser Met Glu
4130 4135 4140

Thr Val Val Gln Glu Met Cys Leu Gly Ile Leu Gln Asn Leu Pro
4145 4150 4155

Thr Asp Ile Asn Leu Glu Asp Val Lys Lys Ile Leu Tyr Arg Lys
4160 4165 4170

Asn Lys Asn Ile Gln Pro Asn Met Gln Thr Asn Thr Gln Leu Asn
4175 4180 4185

Val Thr Cys Asn Leu Gly Ala Thr Thr Lys Asn Phe Gly Ile Leu
4190 4195 4200

Glu Asn Ser Ser Tyr Lys Gly Lys Asn Arg Asp Tyr Asn Ile Asp
4205 4210 4215

Thr Asn Asp Asn Val Asn Asn Asn Ile Leu Gln Lys Ser Val Met
4220 4225 4230

Leu Asn Asn Pro Asn Asn Tyr Thr Ala Asn Val Gly Lys Tyr Ile
4235 4240 4245

Ile Pro Gly Asp Asn Lys Asn Lys Asn Leu Gly Leu Val Lys Glu
4250 4255 4260

Asn Glu Leu Ser Leu Asp Ile Pro Asp Ile Ala Tyr Trp Glu Asn
4265 4270 4275

Asp Asn Glu Gly Glu Lys Asn Val Gln Tyr Asn Phe Ser Pro Leu
4280 4285 4290

Gln Val Phe Phe Leu Gln Glu Met Glu Arg Ile Lys Lys Val Ile
4295 4300 4305

Asp Leu Val Lys Val Asn Leu Asn Asp Ile Ile Ser Ala Ile Asp
4310 4315 4320

Gly Ser Lys Ile Met Thr Ala Asp Leu Gln Asn Asp Thr Lys Tyr
4325 4330 4335

Ile Phe Ser Gln Ser Val Pro Lys Lys Trp Ile Tyr Asp Ala Ser
4340 4345 4350

Glu Thr Glu Ile Ser Trp Ile Cys Asn Asn Leu Asn Gln Trp Leu
4355 4360 4365

Asn Ile Leu Asn Leu Arg Tyr Glu Gln Ile Met Asn Tyr Ile Tyr
4370 4375 4380

Asn Gly Lys Leu Lys Ser Tyr Trp Leu Pro Gly Phe Phe Asn Pro
4385 4390 4395

Gln Gly Phe Leu Thr Ser Met Lys Gln Glu Ile Thr Arg Leu Asn
4400 4405 4410

Lys Lys Asp Gln Leu Ser Leu Asp Glu Val Val Leu Tyr Thr Asp
4415 4420 4425

Ile Lys Asn Tyr Asp Val Glu Lys Ile Lys Glu Phe Pro Glu His
4430 4435 4440

Gly Phe Asn Ile His Gly Leu Phe Ile Glu Gly Ser Lys Trp Asn
4445 4450 4455

Trp Gln Glu Gly Lys Leu Glu Glu Ser Ser Pro Lys Ile Leu Cys
4460 4465 4470

Glu Asn Met Pro Val Ile His Ile Thr Val Val Ser Asn Lys Asp
4475 4480 4485

Lys Lys Ile Lys Phe Ile Glu Asn Asn Lys His Met Phe Tyr Asn
4490 4495 4500

Cys Pro Val Tyr Lys Tyr Asn Val Arg Thr Asp Lys Tyr Phe Ile
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Phe Arg Ile His Leu Lys Ser Asp Ile Asp Pro Ser Ile Trp Lys
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Leu Arg Gly Thr Ser Leu Leu Cys Ser Lys Asp
4535 4540

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Asn Tyr Ser Lys Asn Asn Tyr Gly Leu Asn Asp Gln Glu Leu Arg Ala
35 40 45

Met Leu Phe Gly Leu Asn Tyr Asp Pro Ser Lys Arg Asn Lys Asn Asn
50 55 60

Lys Val Asn Arg Asp Val Ile Lys Asn Glu Ser Ser Leu Leu Leu Arg

65 70 75 80

Asn Leu Ile Asn Glu Glu Thr Leu Ser Glu Lys Asn Asp Lys Val Val
85 90 95

Asn Asp Ile Lys Asn Met Asn Asn Ser Thr Glu Lys Lys Ile Asn Ser
100 105 110

Ile Ser Lys Gly Asn Asn Asn Ile His Asn Ile Asn Glu Asn Gln Asn
115 120 125

Ala Asn Val Glu Leu Lys Thr Asp Asn Ile Leu Asp Asn Thr Ser Glu
130 135 140

Gln Asp Asp Ile Asn Glu Lys Asn Asn Asp Asn Gly Asp Met Val His
145 150 155 160

Lys Asn Ile Tyr Asn Asn Ile Leu Ser Asp Pro Tyr Asp Ile Asn Ser
165 170 175

Thr Asn Ala Tyr Ile Asn Lys Ser Asp Ile Thr Asn Leu Asn Tyr Ser
180 185 190

Ser Asn Asp Val Ile Asn Asn Asp Lys Val Asn Lys Ser Tyr Glu Glu
195 200 205

Lys Asn Ile Val Asn Asn Thr Glu Leu Asn Lys Leu Ile Glu Ser Asp
210 215 220

Asp His Ser Asn Lys Asn Asp Ile Asn Lys Lys Thr Glu Lys Asn Lys
225 230 235 240

Thr Phe Asn Ser Ser Ser Thr Ser Asp Glu Lys Lys Gln Thr Asp Ile
245 250 255

Lys Gly Gln Asn Lys Asn Asp Leu Asn Asn Glu His Ile Phe Asn Asn
260 265 270

Asn Asp Ile Asn Asn Asn Val Gln Tyr Lys Asn Lys Val Asn Ile Ile
275 280 285

Ser Val Asp Lys Asn Asn Thr Asp Arg Asp Asn Asn Asn Leu Tyr Glu
290 295 300

Thr Asn Asn Gly Asp Leu Lys Tyr Asn Asn Asp Leu Ile Lys Glu Gly

305 310 315 320

Glu Asn Lys Arg Asn Asn Lys Leu Asn Asn Tyr Lys Phe Asn Met Asn
325 330 335

Lys Val Asn Asp Asn Lys Asn Phe Asn Lys Tyr Thr Glu Ile Tyr Asn
340 345 350

Lys Glu Ser Glu Pro Glu Lys Gln Asn Asn Ser Asn Asn Asn Leu Gly
355 360 365

Ile Pro Thr Leu Ile Lys Lys Glu Val His Ile Lys Asn His Asn Thr
370 375 380

Phe Ser Ser Asn Gly Lys Ile Leu Glu Asn Lys Asp Ile Asp Lys Met
385 390 395 400

Ser Asp Thr Ser Lys Lys Asn Asp Arg Asn Phe Arg Ser Asn Asp Ile
405 410 415

Lys Asn Phe Lys Asn Asn Asp Thr Lys Asn Asn Ala Thr Leu Ser Glu
420 425 430

Asp Asn Lys Asn Arg Tyr Asn Ile Thr Thr Asn Lys Asn Asn Glu Lys
435 440 445

Lys Glu Tyr Asn Met Lys Lys Ser Asn Glu Asn Glu Tyr Ala Phe Asn
450 455 460

Thr Glu Lys Thr Asn Val Asn Asn Asp Ala Leu Lys Glu Glu Arg Asn
465 470 475 480

Asn Tyr Lys Tyr Leu Asn Asn Gln Thr Asp Val Asn Ile Asn Asn Leu
485 490 495

Gln Glu Arg Asp Ile Asn Leu Tyr Asn Lys Asn Glu Ser Asp Lys Lys
500 505 510

Leu Glu Gln Ser Phe Arg Glu Glu Asp Ile Lys Asn Ala Tyr Leu Pro
515 520 525

Glu Asn Lys Asn Phe Gln Lys Thr Leu Thr Asn Asn Glu Lys Asn Glu
530 535 540

Asp Asn Lys Ile Pro His Ile Asp Pro Ser Asn Asn Glu Leu Asp Lys
545 550 555 560

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Lys Gly Asn Tyr Asn Lys Tyr Glu Ile Gly Lys Ile Lys Lys Asn Asn
                565                 570                 575

Glu Glu Asn Lys Gln Asn Val Thr Val Glu Glu Asn Ile Asn Pro Glu
            580                 585                 590

Lys Ile Arg Lys Asp His Glu Gln Asn Ile Gln Tyr Ser Lys Asn Asp
        595                 600                 605

Pro Ile Thr Asp Ile Gln Asn Ser Thr Asn Ala Val Leu Lys Lys Ile
    610                 615                 620

Lys Pro Thr Glu Phe Glu Asn Tyr Thr Lys Glu Glu Leu Gln Asn Val
625                 630                 635                 640

Ser Ser Ser Glu Val Arg Asp Asp Asn Leu Asn Glu Ile Asn Arg Lys
                645                 650                 655

Gly Glu Thr Asn Met Phe Ser Glu Lys Ser Thr Leu Lys Lys Gly Glu
            660                 665                 670

Asn Asp Trp Asn Glu Tyr Glu Tyr Phe Lys Leu Lys Ser Asn Glu Leu
        675                 680                 685

Lys Val Leu Gly Ile Ile Asn Lys Tyr Ser Pro Lys Gly Gly Phe Ser
    690                 695                 700

Ile Ser Val Asn Cys Gly Gly Tyr Asp Asp Phe Arg Glu Ile Pro Gly
705                 710                 715                 720

Ile Ser Asn Leu Leu Arg His Ala Ile Phe Tyr Lys Ser Glu Lys Arg
                725                 730                 735

Ile Thr Thr Leu Leu Ser Glu Leu Gly Lys Tyr Ser Ser Glu Asn Asn
            740                 745                 750

Ser Arg Ile Gly Glu Ser Phe Thr Thr Tyr Tyr Ala Ile Gly Lys Ser
        755                 760                 765

Glu Asn Ile Tyr Asn Ile Leu Thr Leu Phe Ser Gln Asn Leu Phe Tyr
    770                 775                 780

Pro Leu Phe Asp Glu Asp Phe Ile Glu Asn Glu Val Arg Glu Ile Asn
785                 790                 795                 800
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Asn Lys Tyr Ile Ser Met Glu Asn Asn Ser Leu Asn Cys Leu Lys Ile
805 810 815

Ile Ser Gln Phe Ile Thr Asp Leu Lys Tyr Ser Lys Phe Phe Phe His
820 825 830

Gly Asn Tyr Ile Thr Leu Cys Asn Asn Val Leu Lys Asn Gly Leu Asn
835 840 845

Ile Lys Lys Leu Leu Tyr Asn Phe His Lys Lys Cys Tyr Gln Pro Lys
850 855 860

Asn Met Ala Leu Thr Ile Leu Leu Gly Lys Lys Gly Asn Ser His Asp
865 870 875 880

Asn Tyr Asn Met Asn Asp Ile Glu Asn Phe Val Ile Asp Ile Phe Glu
885 890 895

Lys Ile Lys Asn Tyr Asp Tyr Val Asn Glu Ser Asn Asn Lys Arg Gln
900 905 910

Lys Glu Lys His Ile Val Asn Phe Lys Asp Asp Thr Phe Asn Ile Glu
915 920 925

Lys Lys Ser Asn Tyr Lys Asp Ser Arg Leu Val His Asn Val Thr Gln
930 935 940

Asn Asn Ser Lys Asp Lys Glu Glu Lys Ile Lys Phe Ile Glu His Ile
945 950 955 960

Asn Glu Phe Asn Asn Tyr Val Leu Asp Leu Asn Gln Lys Gly Arg Tyr
965 970 975

Ile Glu Val Leu Lys Lys Glu Gly Trp Arg Asp Gln Ile Tyr Leu Tyr
980 985 990

Trp Ser Ser Lys Ile Ser Ile Asp Leu Tyr Lys Lys Ile Glu Glu Tyr
995 1000 1005

Gly Ser Ile Thr Phe Ile His Asp Ile Leu Leu Asp Leu Arg Lys
1010 1015 1020

Asn Gly Leu Tyr Asp Lys Ile Cys Val Glu Asn Gln Tyr Ala Tyr
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Asp Leu Lys Ile Ile Ser Ser Cys Asn Lys Tyr Tyr Val Asn Tyr
1040 1045 1050

Gly Ile Leu Met Asn Leu Thr Lys Lys Gly Lys Lys Asp Leu Arg
1055 1060 1065

His Leu Met His Ile Ile Asn Val Phe Ile Lys Glu Ile Ser Lys
1070 1075 1080

Leu Phe Asp His Asp Ser Leu Asn Lys Gly Ile Asn Lys Tyr Ile
1085 1090 1095

Leu Asp Tyr Tyr Arg Glu Lys Ala Leu Ile Thr Asp Val Asn Tyr
1100 1105 1110

Asn Asn Asp Asn Lys Tyr Ile Glu Leu Asn Asp Leu Ile Asn Tyr
1115 1120 1125

Ser Asn Ile Leu Leu Asp His Ser Asp Asp Ser Ser Leu Ile Leu
1130 1135 1140

Ser Ile Asn Asn Leu Ile Glu Asp Lys Asn Lys Asn Asp Phe Arg
1145 1150 1155

Asn His Ile Lys Ile Thr Ser Leu Leu Gly Ser Leu Met Lys Asn
1160 1165 1170

Glu Asn Thr Asn Ile Ile Asn Val Val Asp Thr Phe Ser Ile Arg
1175 1180 1185

Asn Gln Ser Lys Ile Pro Tyr Ser Asn Val Thr Tyr Val Ile Gly
1190 1195 1200

Glu Asn Pro Tyr Met Val Asn Glu Gly Asn Ile Val Asn Asp Ile
1205 1210 1215

Asn Leu Ile Leu Pro Glu Ile Lys Ile Cys Pro Phe Asn Ser Leu
1220 1225 1230

Val Asn Asn Lys Ile Leu Phe Asn Glu Lys Ser Phe Phe Cys Val
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Pro Tyr Asn Ser Ser Glu Asn Phe Glu Tyr Ser Glu Ser Glu Glu
1250 1255 1260

Lys Phe Ile Ser Glu Glu Asn Lys His Ile Phe Lys Ser Asn Ile
1265 1270 1275

Leu Tyr Asn Ile Pro Cys Leu Ile Lys Ser Ser Tyr Gly Tyr Asn
1280 1285 1290

Ile Tyr Phe Lys Arg Gly Leu Thr His Ile Ser Lys Val Lys Thr
1295 1300 1305

Asp Phe Ile Phe Tyr Phe Pro Ser Glu Lys Phe Thr Phe Tyr Glu
1310 1315 1320

Ser Val Phe Thr Arg Ile His Ile Ile Ile Leu Gln Lys Lys Ile
1325 1330 1335

Glu Arg Phe Leu Ser Asp Tyr Thr Thr Cys Ser Val Asn Ala Asn
1340 1345 1350

Ile Met His Asp Ala Ile Ser Tyr Thr Leu Ser Ile Glu Ser Asn
1355 1360 1365

Gly Tyr Phe Phe Glu Glu Phe Phe Asn Lys Ile Gln Glu Leu Leu
1370 1375 1380

Ser Leu Lys Glu Ile Pro Ser Arg Asp Glu Tyr Asn Glu Ala Tyr
1385 1390 1395

Asp Glu Leu Asn Ile Ile Ile Gln Thr Asp Thr Thr Ser Gly Val
1400 1405 1410

Asp Lys Ser Leu Lys Ile Met Tyr Ser Leu Phe Asn Lys Tyr Thr
1415 1420 1425

Pro Thr Asn Lys Glu Met Tyr Asp Ile Leu Asn Ala Tyr Phe Phe
1430 1435 1440

Tyr Pro Ser Tyr Asn Ala Tyr Arg Thr Tyr Val Asn Glu Tyr Phe
1445 1450 1455

Leu Arg Asn Tyr Val Val Ile Phe Ile Tyr Gly Asn Ile Ile Ile
1460 1465 1470

Ser Asp Leu Lys Gly Glu Glu Asn Ile Thr Lys Asn Asn Asn Asn
1475 1480 1485

Ile Phe Asp Asn Lys Lys Ser Met Asn Tyr Asn Glu Gly Asp Ala
1490 1495 1500

Thr Asp Lys Asn Asn Asn Ser Asn Asn Asn Asn Val Glu Ser Ala
1505 1510 1515

Asn Asp Ser Thr Asn Tyr Tyr Ile Tyr Asn Glu Asn Asn Ser Ser
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Asn Arg Asp Thr Asn Lys Tyr Thr Asp Asn Asp Tyr Asn Asn Asn
1535 1540 1545

Asn Asn Asn Asn Asn Asn Asn Lys Asp Gly Asp Lys Tyr Leu Ile
1550 1555 1560

Asn Glu Lys Ile Tyr Glu Gly Glu Glu Asn Lys Lys Asn Pro Thr
1565 1570 1575

Thr Tyr Leu Lys Lys Gln Glu Gln Phe Leu Glu Lys Gln Glu Asn
1580 1585 1590

Asn Asn Lys Glu Glu Glu Asn Lys Ser Lys Ser Leu Gln Ile Ser
1595 1600 1605

Tyr Asn Gly Ser Gly Ile Glu Tyr Leu Val Lys Leu Cys Glu Ser
1610 1615 1620

Phe Ile Ser Lys Val Thr Asn Lys Val Ile Lys Lys Ser Glu Ser
1625 1630 1635

Thr Tyr Tyr Thr Lys Lys Leu Ile Asn Asp Glu Asp Ile Glu Ile
1640 1645 1650

Asp Met His Asp Pro Gly Gln Asp Leu Ser Asn Ser Ile Thr Val
1655 1660 1665

Ser Tyr Ile Ile Asp Ser Glu Thr Leu Leu Asn Asn Val Leu Ile
1670 1675 1680

Asn Ile Ile Val Asp Leu Ile Ser Ser Asp Phe Ile Lys Phe Val
1685 1690 1695

Lys Ile Lys Tyr Asn Asp Gly Tyr Val Val Glu Val Arg Thr Phe
1700 1705 1710

Phe Thr Tyr Asn Gly Leu Gly Gly Leu Leu Phe Ile Ile Gln Ser

1715 1720 1725

Phe Asp Lys Asp Val Glu Gln Leu Glu Ser Asp Ile Cys Thr Phe
1730 1735 1740

Val Lys Tyr Ile Thr Phe Gln Leu Leu Asn Ile Asp Ile Ser Asp
1745 1750 1755

Leu Lys Lys Gln Leu Gln Asn Met Lys Glu His Tyr Ile Met Asn
1760 1765 1770

Asn Thr Ile Phe Thr Phe Asn Gln Glu Tyr Ser Ser Ile Leu Asp
1775 1780 1785

Glu Leu Ile Thr Gly His Glu Cys Phe Asp Lys Lys Tyr Lys Ile
1790 1795 1800

Val Gln Ile Phe Asp Glu Leu Ile Asn Cys Pro Asn Ile Ile Leu
1805 1810 1815

Asn Lys Ile Asn Tyr Ile Leu Arg Lys Ser Lys Lys Asn Ile Phe
1820 1825 1830

Lys Glu Tyr Lys Lys Thr Asn Ile Val Asn Ile Gln Ser Ser Asn
1835 1840 1845

Lys Asp Gly Thr Lys Gly His Asp Tyr Leu His Leu Asn Glu Lys
1850 1855 1860

Cys Asn Tyr Ser Tyr Arg Lys Asn Met Lys Met Ser Asn Ile Gln
1865 1870 1875

Phe Ser Asp Asn Ser Glu Leu Phe Ile Lys Lys Gln Arg Lys Lys
1880 1885 1890

Lys Tyr Lys Tyr Ile Pro Ser Asn Gly Thr Thr Gln Ser Asn Asn
1895 1900 1905

Ile Tyr Lys Lys Glu His Leu Phe Asn Phe Ser Asn Phe Val Glu
1910 1915 1920

Ile Lys Glu Lys Gly Phe Phe Lys Tyr Ile Ile Ser Tyr Phe Arg
1925 1930 1935

Lys Asn Asn Arg Lys Tyr Leu Asn Asp Asp Asn Tyr Leu Asp Phe
1940 1945 1950

Glu Ser Cys Asp Glu Glu Met Ser Lys Asp Asn Phe Gln Ile Phe
1955 1960 1965

Tyr Asn Phe Thr Asn Asp Ile Asn Lys Ile Arg Glu Tyr Phe Arg
1970 1975 1980

Gly Lys Phe Thr Asn Asp Lys Glu Val Lys Glu Asn Cys Ser Ile
1985 1990 1995

Asn Tyr Glu Glu Ile Arg Lys Tyr Cys Tyr Asp His Asn Ile Asn
2000 2005 2010

Lys Asp Asn Met Ile Arg Thr Lys Ile Glu Ile
2015 2020

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Ile Ile Tyr Lys Arg Phe Asn Tyr Ile Ser Ser Asn Gly Lys Leu Asn
35 40 45

Tyr Asp Asn Phe Glu Lys Ser Leu Gly Ile Leu Gly Ser Ile Gln Asn
50 55 60

Ala Tyr Leu Tyr Lys Ser Ile Phe Lys Ala Phe Asp Leu Asn Asn Asp
65 70 75 80

Asn Tyr Leu Asp Phe Tyr Glu Phe Cys Val Ala Ile Asn Ile Met Leu
85 90 95

Lys Gly Asn Lys Lys Asp Lys Leu Lys Leu Ser Tyr Arg Ile Val Asn
100 105 110

Ala Gly Phe Asn Ser Asn Glu Asp Ala Cys Val His Lys Ser Ser Cys
115 120 125

Met Val Asn Lys Phe Asn Thr Lys Glu Asp Asn Asn Met Asn Gly Asp
130 135 140

Asn Ile Asn Gly Asp Asn Asn Asn Asn His Asn Asn Ile Asn Gly Asp
145 150 155 160

Asn Asn Asn Asn His Asn Asn Ile Asn Gly Asp Asn Asn Asn Asn Asn
165 170 175

His Asn Asn Ile Asn Gly Asp Asn Asn Asn Asn His Asn Asn Ile Asn
180 185 190

Gly Asp Asn Asn Asn Asn Asn His Asn Asn Ile Asn Gly Asp Asn Asn
195 200 205

Asn Asn His Asn Asn Ile Asn Gly Asp Asn Asn Asn Asn His Asn Asn
210 215 220

Ser His Asn Asn Asn Ser His Asn Asn Asn Asn Lys Ala Glu Asn Ser
225 230 235 240

Leu Gly Gln Pro Leu Asn Glu Lys Asn Ile Asn Asp Pro Ile Asn Lys
245 250 255

His Arg Asn Ser Gln Ser Ile Ile Tyr Asn Ile Asn Asp Glu Tyr Asn
260 265 270

Glu Lys Ile Lys Lys Asn Lys Lys Gln Asp Tyr Ser Asn Tyr Ile Thr
275 280 285

Tyr Glu Asn Phe Glu Lys Ile Val Leu Ser Ile Asn Asp Ile Lys Arg
290 295 300

Gln Leu Leu Gly Thr Gly Asp Glu Ile Ile Thr Ser Gln Ile Lys Tyr
305 310 315 320

Thr Phe Arg Ser Leu Ser Ile Leu Cys Asp Asp Gly Ile Tyr Arg Met
325 330 335

Asn Phe Glu Cys Tyr Lys Lys Ala Leu Lys Cys Asn Glu Phe Leu Lys
340 345 350

Leu Leu Gly Ile His Thr Lys Val Ala Asp Val Phe Leu Gln His Glu
355 360 365

Leu Leu Lys Arg Lys Asp Lys Asn Lys Thr Lys Asn Gly Thr Met Arg

370 375 380

Asn Arg Lys Lys Tyr Lys Asn Asp Ser Asn Arg Ile Ala Asn His Leu
385 390 395 400

Ile Ile Lys Ser Phe Ser Glu Ser Thr Asn Thr Arg Gly Ser Ile Ile
405 410 415

Asn Asp Ser Thr Ser Phe Leu Phe Leu Arg Lys Gln Lys Lys Lys Lys
420 425 430

Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Glu Lys Lys Ala Ile Leu
435 440 445

Tyr Glu Arg Lys Ser Thr Phe Ser Ser Ser Met Glu Asn Lys Ser Gln
450 455 460

Asn Lys Ser Gln Asn Lys Ser His Asn Lys Asn Ile Lys Ser Val Ser
465 470 475 480

Arg Ile Leu Ser Arg Val Asn Lys Leu Ser Ser Thr Glu Leu Ile Pro
485 490 495

Asn Glu Cys Asp His Lys Pro Asn Glu Glu Val Lys Ser Thr Ser Asp
500 505 510

Val Leu Thr Pro Ile Phe Phe Asn Asn Gly Asp Glu Lys Met Asn His
515 520 525

Asp Thr Asp Gly Asn Met Val Tyr His Lys Asn Asn Val Asp Asp Asn
530 535 540

Leu Val Asp Gly Asp Val Val Ser Gln Gly Lys Arg Cys Ser Phe Phe
545 550 555 560

Ser Ser Cys Glu Asn Lys Lys Asn Glu Glu Asn Lys Ser Ile Thr Phe
565 570 575

Asn Asp Ile Asn Ser Gly Asn Ile Asn Thr Asn Ser Cys Ile Met Asn
580 585 590

Asn Met Ile Val Thr Lys Glu Ser Asn Glu Glu Ile Ile Asn Glu Glu
595 600 605

Ala Gln Ser Ser Tyr Ile Tyr Asn Lys Asn Ile Phe Cys Ser Lys Tyr
610 615 620

Asn Thr Lys Lys Asp Lys Asn Glu Pro Leu Lys Cys Asp Leu Phe Glu
625 630 635 640

Cys Ser Phe Ile Asn Asn Asp Lys Asn Ile Val Arg Asp Glu Asp Ser
645 650 655

Asn His Lys Asn Val Arg Lys Thr Asp Asp Tyr Phe Ile Ile Asp Asp
660 665 670

Asn Asn Ile Phe Asp Asn Gly Pro Ile Ile Ile Ser Lys Asn Lys Thr
675 680 685

Asn Asp Arg Glu Arg Lys Leu Leu Lys Thr Phe Ser Ser Ser Ser Leu
690 695 700

Lys Lys Lys Ser Leu Leu Lys Asn Tyr Asn Tyr His Ile Lys Lys Lys
705 710 715 720

Asn Lys Asp Pro Asn Val Glu Asp Thr Asn Met Leu Tyr His Asp Asp
725 730 735

Ile Lys Lys Glu Tyr Asp His Lys Val Thr Lys Asn Asn Lys Asn Thr
740 745 750

Cys Asn Asn Asn Tyr Tyr Asn Asn Val Ser Phe Asn Ser Ser Ala Tyr
755 760 765

Tyr Glu Tyr His Ser Asp Ile Asp Leu Ile His Phe Ser Asn Asn Leu
770 775 780

Lys Lys Lys Lys Lys Lys Asn Val Thr Ser Pro Arg Pro Ser Ser Lys
785 790 795 800

Glu Tyr Glu Arg Lys Val Thr Tyr His Lys Glu Cys Cys Ser Asn Glu
805 810 815

Arg Met Lys Asn Ile Lys Val Asn Glu Ser Asp Leu Gly Met Phe Cys
820 825 830

Val Asn Asn Asp Lys Thr Asn Ile Glu Asp Val Lys Glu Lys Lys Ala
835 840 845

Cys Asp Val Leu Asn Arg Gly Cys Ile Lys Glu Gln Val Gln Cys Lys
850 855 860

Ile Ser Glu Phe Glu Asn Asp Lys Gly Asn Glu Ile Tyr Met Gln Glu
865 870 875 880

Phe Lys Lys Cys Ile Glu Lys Tyr Lys Glu Tyr Val Asn Gln Gly Glu
885 890 895

Gly His Leu Lys Asp Glu Glu Glu Glu Lys Asn Asp Asp Glu Glu Glu
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Gly Glu Asp Gly Glu Asp Asp Glu Glu Glu Asn Asp Asp Asp Asp Asp
915 920 925

Asp Glu Asp Gly Asp Asp Asp Glu Asp Gly Asp Asp Asp Asn Asp Asp
930 935 940

Asn Asp Asp Asn Asp Asp Asn Asp Asp Asn Asp Asp Asn Asp Asp Asn
945 950 955 960

Asp Asp Asn Asp Asp Asn Asp Asp Asn Asp Asp Asn Asp Glu Lys Ser
965 970 975

Asn Ile Lys Ile Glu Asn Lys Lys Asp Val Pro Asn Ile His Asn Asn
980 985 990

Asn Asp Asp Asp Gly Ile Asn Cys Cys Thr Asn Leu Phe Lys Asp Asp
995 1000 1005

Asp Thr Leu Ser Ala Leu Glu Lys Asn Val Thr Asn Asn Asn Leu
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Ile Lys Ile Met Ser Ala Lys Tyr Leu Tyr His Lys Phe Leu Glu
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Tyr Lys Asp Phe Met Lys Asn Asn Thr Thr Leu Phe Ser His Phe
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Asn Lys Ile Tyr Gln His Glu Asp Asp Lys Ile Asn Thr Asp Asn
1055 1060 1065

Lys Asp Val Leu Asn Tyr Arg Pro Lys His Asn Asn Asp Ile Asn
1070 1075 1080

Tyr Tyr Asn Ile Pro Cys Glu Asp Gln Ile Lys Ser Asp Glu Lys
1085 1090 1095

Lys Ser Leu Leu Asn Val Glu Phe Gly Asp Asp Ile Ile Lys Lys
1100 1105 1110

Lys Phe Phe Ile Ser Ser Val Asn Ser His Tyr Val Met Ile Asn
1115 1120 1125

Asn Asn Leu Thr Lys Glu Gln Met Leu Tyr Leu Ile Arg Asn Ile
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Leu Met Ser Ile Glu Asp Tyr Leu Lys Lys Glu Lys Asn Arg Asp
1145 1150 1155

Tyr Asn Lys Ile Phe Phe Leu Phe Phe Ser Ile Phe Ile Tyr Asn
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Thr Gln Asn Gly Gly Asp Gln Lys Glu Met His Glu Asp Glu Lys
1175 1180 1185

Trp Asp His Thr Asn Ile Asn Glu Asp Lys Asn Val Glu Lys Asn
1190 1195 1200

Asp Asp Tyr Lys Asn Leu Ser Asn Asn Glu Asn Ser Val Tyr Tyr
1205 1210 1215

Asn Thr Met Leu Arg Glu Ser Leu Trp Asn Lys Lys Lys Tyr Ile
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Lys Leu Asn Ile Phe Lys Asn Ile Ile Leu Val Ile Ser Ile Val
1235 1240 1245

Arg Tyr Phe Leu His Thr Ile Thr Ile Ser Gln Lys Tyr Thr Ser
1250 1255 1260

Ser Tyr Asp Ser Leu Asp Asp Ser Asn Met Ile Lys Ser Met Asn
1265 1270 1275

Ser Leu Lys Leu Asn Glu Ile Asn Ile Leu Leu Asn Arg Ala Ser
1280 1285 1290

Glu Ile Leu Glu Lys Tyr Ser Leu Gly Ser Val Glu Asn Lys Lys
1295 1300 1305

Val Tyr Ile Asn Lys Ser Asn Tyr Tyr Asn Ser Ser Lys Lys Gly
1310 1315 1320

Lys Leu Ser Val Ser Leu Arg Gln Asn Lys Gln Lys Lys Thr Phe

1325 1330 1335

His Arg Ile Leu Ala Val Tyr Phe Gly His Glu Arg Trp Asp Leu
1340 1345 1350

Val Met Asn Met Met Ile Gly Ile Arg Ile Ser Ser Ile Lys Lys
1355 1360 1365

Phe Ser Ile Asn Asp Ile Ser Asn Tyr Phe His His Lys Asp Val
1370 1375 1380

Ile Gln Leu Pro Thr Ser Asn Ala Gln His Lys Val Ile Phe Lys
1385 1390 1395

Asn Tyr Ala Pro Ile Ile Phe Lys Asn Ile Arg Asn Phe Tyr Gly
1400 1405 1410

Ile Lys Ser Lys Glu Tyr Leu Thr Ser Val Gly Pro Glu Gln Val
1415 1420 1425

Ile Ser Asn Met Val Leu Gly Asn Leu Ser Thr Leu Ser Glu Leu
1430 1435 1440

Leu Ser Glu Gly Lys Ser Gly Ser Leu Phe Tyr Phe Thr Ser Asn
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Gly Lys Tyr Ile Ile Lys Thr Val Ile Lys Lys Lys Lys
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Leu Asp Glu Ile Gly Glu Thr Ile Gln Lys Lys Ala His Ser Asp Ala
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Asp Thr Phe Arg Ser Gln Leu Lys Gly Asn Phe Gly Glu Ala Lys Phe
35 40 45

Tyr Asn Gly Gly Glu Ile Met Gln Pro Asn Ser Lys Leu Cys Glu Leu
50 55 60

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Asp His Thr Ile Asp Thr Asn Val Thr Asp Gly His Ser Asn Pro Cys
65                  70                  75                  80

Glu Gly Arg Gln Thr Val Arg Phe Pro Asp Asp Asn Arg Ser Gln Cys
                85                  90                  95

Thr Lys Asn Arg Ile Lys Asp Ser Val Asp Asn Ser Val Gly Ala Cys
            100                 105                 110

Ala Pro Tyr Arg Arg Leu His Leu Cys Ser His Asn Leu Glu Ser Ile
        115                 120                 125

Gln Thr Asn Asn Tyr Asp Ser Ser Lys Ala Lys His Asn Leu Leu Ala
    130                 135                 140

Glu Val Cys Tyr Ala Ala Lys Phe Glu Gly Glu Ser Ile Val Lys Asn
145                 150                 155                 160

Tyr Glu Gln Leu Gly His His Thr Thr Glu Gly Ile Cys Thr Ala Leu
                165                 170                 175

Ala Arg Ser Phe Ala Asp Ile Gly Asp Ile Ile Arg Gly Lys Asp Leu
            180                 185                 190

Tyr Leu Gly Asn Pro Gln Glu Ser Ala Arg Arg Lys Gln Leu Glu Asp
        195                 200                 205

Asn Leu Arg Lys Ile Phe Glu Lys Ile Tyr Lys Glu Leu Thr Ser Ser
    210                 215                 220

Arg Asn Gly Lys Thr Asn Gly Ala Glu Glu Arg Tyr Lys Asp Gly Ser
225                 230                 235                 240

Gly Asn Tyr Tyr Lys Leu Arg Glu Asp Trp Trp Asn Ala Asn Arg Leu
                245                 250                 255

Asp Ile Trp Lys Ala Met Ile Cys Lys Ala Pro Gly Asn Ala Pro Tyr
            260                 265                 270

Phe Arg Asn Thr Cys Ser Asn Gly Glu Lys Pro Thr Gly Glu Lys Cys
        275                 280                 285

Gln Cys Ile Asp Gly Thr Val Pro Thr Asn Leu Asp Tyr Val Pro Gln
    290                 295                 300
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Tyr Leu Arg Trp Phe Glu Glu Trp Ala Glu Glu Phe Cys Arg Lys Arg
305                 310                 315                 320

Asn Leu Lys Leu Gln Asn Ala Ile Lys Asn Cys Arg Gly Met Asp Asp
                325                 330                 335

Asp Gly Lys Glu Lys Tyr Cys Ser Arg Asn Gly Tyr Asp Cys Thr Lys
            340                 345                 350

Thr Ile Arg Ser Ile Asp Lys Tyr Ser Met Asn Arg Glu Cys Thr Lys
        355                 360                 365

Cys Leu Tyr Val Cys Asp Pro Tyr Val Lys Trp Ile Asp Asn Lys Lys
    370                 375                 380

Lys Glu Phe Glu Lys Gln Lys Lys Lys Cys Glu Asn Glu Ile Tyr Arg
385                 390                 395                 400

Asn Asn Glu Ser Ser Gln Asn Ser Pro Lys Asn Tyr Asn Asn Met Tyr
                405                 410                 415

Glu Thr Asp Phe Tyr Gly Asn Leu Lys Lys Asp Tyr Gln Ser Met Asn
            420                 425                 430

Asp Phe Leu Lys Leu Leu Asn Ser Glu Thr Pro Cys Thr Asn Ile Ile
        435                 440                 445

Asp Ala Lys Ser Lys Ile Asp Phe Thr Lys Asp Pro Glu Glu Thr Phe
    450                 455                 460

Ser His Thr Glu Tyr Cys Asp Pro Cys Pro Trp Cys Gly Leu Lys Thr
465                 470                 475                 480

Gln Ala Asp Gly Thr Trp Lys Arg Leu Tyr Glu Asn Asp Pro Gln Cys
                485                 490                 495

Pro Ile Lys Pro Lys Tyr Glu Pro Pro Lys Gly Val Glu Pro Thr Glu
            500                 505                 510

Thr Asp Val Leu Tyr Thr Gly Lys Glu Asn Lys Asp Ile Ile Val Lys
        515                 520                 525

Leu Arg Glu Phe Cys Lys Thr Asp Gly Asn Thr Gly Phe Lys Asn Glu
    530                 535                 540
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Glu Trp Asn Cys Tyr Tyr Gln Val Gly Asn Asp Lys Cys Val Leu Glu
545                 550                 555                 560

Asn Gly Glu Glu Leu Gly Gly Glu Lys Lys Val Lys Asp Tyr Asp Asn
                565                 570                 575

Phe Leu Met Phe Trp Val Ala His Met Leu Lys Asp Ser Ile Glu Trp
            580                 585                 590

Arg Ser Lys Leu Ser Asn Cys Leu Lys Ser Asp Lys Lys Thr Cys Ile
        595                 600                 605

Thr Thr Cys Asn Asp Asn Cys Gln Cys Tyr Asp Lys Trp Ile Gly Lys
    610                 615                 620

Lys Lys Val His Trp Thr Gln Ile Lys Lys His Phe Asp Lys Gln Thr
625                 630                 635                 640

Asp Phe Gln Gly Trp Gly His Tyr Phe Val Leu Glu Thr Val Leu Glu
                645                 650                 655

Gly Asp Gln Phe Phe Thr Asp Ile Thr Lys Ala Tyr Gly Asp Ala Arg
            660                 665                 670

Glu Ile Val His Ile Gln Glu Met Leu Gln Lys Lys Lys Glu Gln Val
        675                 680                 685

Leu His Glu Asp Ala Ser Asn Met Lys Thr Ile Ile Asp Glu Leu Leu
    690                 695                 700

Asp His Glu Leu Lys Glu Ala Lys Gln Cys Ile Val Asn His Lys Asp
705                 710                 715                 720

Asn Asn Cys Pro Ala Asp Leu Ser Asp Ser Glu Asp Glu Glu Glu Asp
                725                 730                 735

Ile Pro Gln Arg Gln Asn Lys Cys Ala Lys Pro Ser Gly Thr His Ile
            740                 745                 750

Arg Ala Leu Val Asn Lys Val Ala Ser Asn Met His His Lys Lys Lys
        755                 760                 765

Arg Gln Leu Val Asn Arg Gly Val Ser Ser Lys Leu Lys Gly Asp Ala
    770                 775                 780

Ala Lys Gly Glu Tyr Arg Lys Ser Gly Thr Thr Ile Lys Leu Lys Asp
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785 790 795 800

Ile Cys Ser Ile Thr Asp Asp His Ser Asn Ala Lys Arg Gly His Thr
805 810 815

Asp Gln Pro Cys Lys Arg Lys Asp Ser Lys Val Asn Val Lys Asn Arg
820 825 830

Arg Trp Met Asp Thr Ala Gly Phe Ile Ser Asn Thr Tyr Lys Asp Ile
835 840 845

Tyr Met Pro Pro Arg Arg Gln His Phe Cys Thr Ser Asn Leu Glu Tyr
850 855 860

Leu Gln Thr Thr Asn Lys Leu Leu Asn Gly Asn Asp Ile Asn Gly Asn
865 870 875 880

Pro Asn Ile Ile Asn Asp Ser Phe Leu Gly Asp Val Leu Phe Ala Ala
885 890 895

Asn Tyr Glu Ala Asp Phe Ile Lys Lys Met Tyr Asn Lys Gln Asn Asp
900 905 910

Tyr Lys Asp Asn Ala Thr Ile Cys Arg Ala Met Lys Tyr Ser Phe Ala
915 920 925

Asp Leu Gly Asp Ile Ile Gln Arg Gln His Ile Cys Arg Ile Met Ile
930 935 940

Val Glu Arg Val Lys His Glu Ile Ser Glu Arg Asn Phe Leu Ile Leu
945 950 955 960

Ser Lys Lys Asn Ile Leu Ala Phe Lys Glu Ile Tyr Lys Glu Asp Thr
965 970 975

Pro Tyr Thr Lys Leu Arg Glu Asp Trp Trp Glu Ala Asn Arg Lys Lys
980 985 990

Ile Trp Glu Ala Met Gln Cys Pro Thr Pro Asn Gly Ser Phe Pro Cys
995 1000 1005

Lys Ser Tyr His Ile Gly Leu Asp Asp Tyr Ile Pro Gln Arg Leu
1010 1015 1020

Arg Trp Met Thr Glu Trp Ala Glu Trp Phe Cys Lys Glu Gln Lys

1025 1030 1035

Lys Gln Tyr Gly Glu Leu Val Ser Ala Ser Asn Gly Cys Lys Asp
1040 1045 1050

Glu Arg Val Lys Val Val Arg Ile Arg Val His Asn Val Gln Arg
1055 1060 1065

Ala Cys Lys His Val Lys Ile Ile Lys Asn Leu Leu Ile His Gly
1070 1075 1080

Lys Glu Gln Trp Asp Lys Met Glu Ile Lys Tyr Lys Leu Leu Tyr
1085 1090 1095

Leu Gln Ala Gln Thr Thr Ala Ala Asn Gly Gly Pro Asp Thr Tyr
1100 1105 1110

Ser Gly Leu Val Asp Glu Asn Glu Lys Pro Val Val Asn Phe Leu
1115 1120 1125

Phe Glu Leu Tyr Lys Glu Asn Gly Gly Lys Ile Gly Asn Pro Arg
1130 1135 1140

Asp Thr Pro Arg Ala Lys Arg Ser Lys Arg Glu Thr Ala Pro Ala
1145 1150 1155

Ser Val Ala Lys Asn Asp Val Tyr Ser Thr Ala Ala Gly Tyr Val
1160 1165 1170

His Gln Glu Met Gly Pro His Met Glu Cys Lys Thr Gln Thr Glu
1175 1180 1185

Phe Cys Glu Lys Thr Asp Glu Gln Tyr Asn Glu Asn Tyr Thr Phe
1190 1195 1200

Lys Asn Pro Pro Pro Gln Tyr Lys Asp Ala Cys Ile Cys Asn Thr
1205 1210 1215

Arg Pro Pro Pro Lys Glu Asp Ser Arg Lys Arg Ser Glu Asp Ser
1220 1225 1230

Asp Glu Glu Glu Lys Val Lys Glu Thr Lys Val Glu Glu Lys Ala
1235 1240 1245

Thr Glu Asp Ala Val Asp Thr Gly Pro Pro Pro Ala Pro Lys Glu
1250 1255 1260

Ala Thr Thr Thr Leu Asp Val Cys Pro Ile Val Ala Gly Val Leu
1265 1270 1275

Thr Lys Glu Asn Leu Glu Asn Ala Cys Pro Thr Lys Tyr Gly Pro
1280 1285 1290

Lys Ala Pro Thr Ser Trp Lys Cys Ile Pro Thr Glu Lys Thr Asn
1295 1300 1305

Ala Ala Thr Gly Ser Glu Gly Ser Ser Gly Asn Gly Ala Leu Gln
1310 1315 1320

Arg Ala Lys Arg Ala Thr Val Glu Ser Gly Ser Pro Val Thr Ser
1325 1330 1335

Asn Ser Gly Ser Ile Cys Ile Pro Pro Arg Arg Arg Arg Leu Tyr
1340 1345 1350

Ile Gln Lys Leu His Asp Trp Ala Ser Gly Asn Thr Val Val Ser
1355 1360 1365

Gly Gln Ala Gln Thr Pro Gln Gly Gly Thr Ser Ser Pro Ser Gly
1370 1375 1380

Lys Glu Thr Pro Ser Asp Lys Leu Arg Thr Ala Phe Ile Gln Ser
1385 1390 1395

Ala Ala Ile Glu Thr Phe Phe Leu Trp Asp Arg Tyr Lys Lys Gly
1400 1405 1410

Lys Ala Ile Ala Lys Lys Glu Lys Lys Lys Gln Met Val Asp Tyr
1415 1420 1425

Ser Pro Leu Ser Thr Ala Asp Pro His Asn Asn Pro Val Ser Leu
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Val Ile Ala Pro Asn Pro Asn Tyr Asn Lys Thr Cys Val Ile Pro
1445 1450 1455

Pro Pro Phe Leu Arg Gln Met Phe Tyr Thr Leu Gly Asp Tyr Ala
1460 1465 1470

Asp Ile Phe Phe Gly Lys Asn Asp Ile Val Ile Asp Thr Lys Asn
1475 1480 1485

Gly Asp Lys Asp Ile Ala Glu Arg Glu Lys Lys Ile Lys Asp Ala
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Ile Glu Arg Val Leu Lys Asn Ala Asp Ser Gln Pro Pro Ser Asp
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Glu Lys Arg Gln Thr Trp Trp Glu Gln Asn Gly Glu His Ile Trp
1520 1525 1530

Asn Gly Met Ile Cys Ala Leu Thr Tyr Lys Glu Lys Asp Glu Lys
1535 1540 1545

Gly Thr Pro Leu Lys Gln Asn Glu Gly Leu Lys Ser Ala Leu Trp
1550 1555 1560

Asp Glu Lys Asn Lys Lys Pro Lys Asp Gln Lys Tyr Gln Tyr Asp
1565 1570 1575

Lys Val Lys Leu Asp Glu Asn Ser Gly Thr Ser Pro Lys Ile Val
1580 1585 1590

Val Pro Ala Pro Lys Pro Thr Thr Thr Phe Pro Pro Pro Pro Ser
1595 1600 1605

Pro Thr Ser Phe Ser Arg Pro Pro Tyr Phe Arg Tyr Leu Glu Glu
1610 1615 1620

Trp Ala Glu Thr Phe Cys Arg Glu Arg Lys Lys Arg Leu Glu Lys
1625 1630 1635

Ile Lys Val Glu Cys Met Asp Glu Asp Gly Lys Lys Gln Lys Cys
1640 1645 1650

Ser Gly Asp Gly Glu Asp Cys Glu Glu Ile Arg Lys Gln Asp Tyr
1655 1660 1665

Ser Thr Val Arg Asp Phe Tyr Cys Pro Glu Cys Gly Lys Tyr Cys
1670 1675 1680

Arg Phe Tyr Lys Arg Trp Ile Gly Lys Lys Lys Asp Glu Tyr Asp
1685 1690 1695

Lys Gln Lys Glu Ala Tyr Asn Asn Gln Lys Thr Asp Ala Arg Arg
1700 1705 1710

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Asn Asn  Asn Asp Asn Ala Phe  Ser Thr Thr Leu Asp  Thr Cys Thr
    1715                 1720                 1725

Thr Ala  Gly Asp Phe Leu Gln  Thr Leu Lys Asn Gly  Pro Cys Lys
    1730                 1735                 1740

Asn Asp  Asn Val Asp Asp Ser  Gly Glu Asn Lys Lys  Ile Phe Asp
    1745                 1750                 1755

Glu Asn  Gly Asp Thr Phe Lys  Tyr Thr Gln Tyr Cys  Gly Thr Cys
    1760                 1765                 1770

Ser Leu  Asn Gly Phe Lys Cys  Asn Gly Asp Asp Cys  Arg Val Arg
    1775                 1780                 1785

Thr Asn  Val Thr Cys Asn Gly  Ser Asn Arg Thr Thr  Thr Ile Thr
    1790                 1795                 1800

Ala Asp  Asp Ile Lys Asn Gly  Gly Asn Ser Ala Glu  Ile Asn Met
    1805                 1810                 1815

Leu Val  Ser Asp Asp Ile Asn  Ser Gly Asn Gly Phe  Asn Asp Leu
    1820                 1825                 1830

Glu Ala  Cys Lys Asn Ala Asn  Ile Phe Lys Gly Ile  Lys Glu Asn
    1835                 1840                 1845

Lys Trp  Lys Cys Val Tyr Phe  Cys Lys Ser Asp Val  Cys Gly Leu
    1850                 1855                 1860

Lys Lys  Asn Asn Asp Ile Asp  Gln Asn Gln Ile Ile  Leu Ile Arg
    1865                 1870                 1875

Ala Leu  Phe Lys Arg Trp Leu  Glu Tyr Phe Leu Asp  Asp Tyr Asn
    1880                 1885                 1890

Lys Ile  Arg Lys Lys Leu Asn  Pro Cys Ile Asn Asn  Gly Glu Lys
    1895                 1900                 1905

Ala Ile  Cys Thr Asn Gly Cys  Val Glu Gln Trp Ile  Asn His Lys
    1910                 1915                 1920

Arg Thr  Glu Trp Thr Asn Leu  Lys Ser Phe Asn Glu  Gln Tyr Asn
    1925                 1930                 1935
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Gly Asp Asp Thr Glu Arg Asn Pro Arg Leu Arg Phe Phe Val Asp
1940 1945 1950

Leu Ile Arg Gln Ile Ala Ala Thr Ile Asp Lys Gly Asn His Asn
1955 1960 1965

Gly Leu Val Lys Leu Val Lys Ser Val Lys Cys Asn Cys Gly Asn
1970 1975 1980

Asn Ser Gln Asn Gly Lys Glu Gly Glu Glu Asn Asp Leu Val Leu
1985 1990 1995

Cys Leu Leu Gln Lys Leu Glu Lys Lys Ala Glu Lys Cys Lys Asp
2000 2005 2010

Asn Pro Glu Thr Ser Gly Ile Pro Gln Gln Pro Cys Glu Val Ser
2015 2020 2025

Pro Asn His Ile Glu Asp Glu Glu Gln Pro Leu Glu Glu Glu Glu
2030 2035 2040

Asn Thr Val Glu His Pro Lys Ile Cys Asp Asp Val Leu Lys His
2045 2050 2055

Asn His Asn Gln Arg Asn Gln Glu Arg Leu Val Lys Asn Pro Leu
2060 2065 2070

Val Gln Pro Thr Leu Lys Arg Lys Lys Lys Lys Lys Lys Arg Arg
2075 2080 2085

Lys Lys Ile Lys Lys Lys Asn Gln Asp Phe His Pro Arg His Leu
2090 2095 2100

Pro Cys Gly Ala Phe Ile Asn Thr Asn Thr Pro Lys Thr Lys Thr
2105 2110 2115

Pro Pro Ser Ser Gly Lys Asn Pro Trp Glu His Pro Ala Val Ile
2120 2125 2130

Pro Ala Leu Val Thr Ser Thr Leu Ala Trp Ser Val Gly Ile Gly
2135 2140 2145

Phe Ala Ala Phe Thr Tyr Phe Tyr Leu Lys Lys Lys Thr Lys Ser
2150 2155 2160

Thr Ile Asp Leu Leu Leu Ser Leu Ile Pro Lys Ser Asp Tyr Asp

2165 2170 2175

Ile Pro Thr Lys Leu Ser Pro Asn Arg Tyr Ile Pro Tyr Thr Ser
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Gly Lys Tyr Arg Gly Lys Arg Tyr Ile Tyr Leu Glu Gly Asp Ser
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Gly Thr Asp Ser Gly Tyr Thr Asp His Tyr Ser Asp Ile Thr Ser
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Ser Ser Glu Ser Glu Tyr Glu Glu Met Asp Ile Asn Asp Ile Tyr
2225 2230 2235

Val Pro Gly Ser Pro Lys Tyr Lys Thr Leu Ile Glu Val Val Leu
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Glu Pro Ser Gly Lys Leu Ser Gly Asn Thr Ile Pro Thr Ser Gly
2255 2260 2265

Asn Asn Thr Thr Ala Ser Asp Thr Gln Asn Asp Ile Pro Thr Ser
2270 2275 2280

Asp Thr Pro Pro Pro Ile Thr Asp Asp Glu Trp Asn Thr Leu Lys
2285 2290 2295

His Asp Phe Ile Ser Asn Met Leu Gln Asn Gln Pro Lys Asp Val
2300 2305 2310

Pro Asn Asp Tyr Thr Ser Gly Asn Ser Ser Thr Asn Thr Asn Ile
2315 2320 2325

Thr Thr Thr Ser Arg Asp Asn Val Asp Asn Asn Thr His Pro Thr
2330 2335 2340

Met Ser Arg His Asn Val Asp Gln Lys Pro Phe Ile Thr Ser Ile
2345 2350 2355

His Asp Arg Asn Leu Tyr Thr Gly Glu Glu Tyr Asn Tyr Asn Val
2360 2365 2370

Asn Met Val Asn Thr Met Asp Asp Ile Pro Ile Asn Ser His Asn
2375 2380 2385

Asn Val Tyr Ser Gly Ile Asp Leu Ile Asn Asp Thr Leu Ser Gly

2390 2395 2400

Asn Glu His Ile Asp Ile Tyr Asp Glu Leu Leu Lys Arg Lys Glu
2405 2410 2415

Asn Glu Leu Phe Gly Thr Asn His Val Lys Gln Thr Ser Ile His
2420 2425 2430

Ser Val Ala Lys Pro Thr Arg Asp Asp Pro Ile His Asn Gln Leu
2435 2440 2445

Glu Leu Phe His Lys Trp Leu Asp Ser His Arg Asp Met Cys Glu
2450 2455 2460

Gln Cys Lys Asn Asp Asn Glu Arg Leu Ala Lys Leu Lys Glu Leu
2465 2470 2475

Trp Glu Asn Glu Thr Gln Cys Gly Asp Ile Asn Ser Gly Ile Pro
2480 2485 2490

Ser Gly Lys Leu Ser Asp Thr Pro Ser Asp Asn Asn Ile His Ser
2495 2500 2505

Asp Ile His Pro Ser Asp Ile Pro Ser Gly Lys Gln Ser Asp Ile
2510 2515 2520

Pro Ser Asp Asn Asn Ile His Ser Asp Ile Pro Tyr Val Leu Asn
2525 2530 2535

Thr Asp Val Ser Ile Gln Ile His Met Asp Asn Pro Lys Pro Ile
2540 2545 2550

Asn Glu Phe Thr Tyr Val Asp Ser Asn Pro Asn Gln Val Asp Asp
2555 2560 2565

Thr Tyr Val Asp Ser Asn Pro Asp Asn Ser Ser Met Asp Thr Ile
2570 2575 2580

Leu Asp Asp Leu Glu Lys Tyr Asn Glu Pro Tyr Tyr Asp Val Gln
2585 2590 2595

Asp Ile Tyr Asn Asp Val Asn Asp Asp Asn Asp Ile Ser Thr Val
2600 2605 2610

Asp Thr Asn Ala Met Asp Val Pro Ser Lys Val Gln Ile Glu Met

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Asp Ile Asn Thr Glu Ile Phe Glu Glu Glu Tyr Pro Ile Ser Asp
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Ile Trp Asn Ile
2645

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Asn Ile Asp Leu Asn Ile Tyr Pro Asn Met Ser Asn Tyr Val Asp Ile
35 40 45

Gly Ser Asn Ile Tyr Val Glu Gln Ile Lys Asn Ile Ser Lys Glu Glu
50 55 60

Val Thr Lys Lys Lys Ser Ile Leu Asn Ser Lys Tyr Ile Ser Ser Lys
65 70 75 80

Asn Asn Glu Phe Val Val Ala Gln Leu Tyr Glu Leu Asn Asn Tyr Asn
85 90 95

Glu Asn Asn Ile Tyr Glu Asp Arg Asn Leu Phe Ser Asn Ser Thr Asn
100 105 110

Ile Tyr Ser Asn Asp Asn Asn Met Lys Lys Tyr Leu Ile Gln Lys Cys
115 120 125

Gly Lys Lys Asn Ile Lys Lys Arg Met Asp Ile Leu Asn Gln Glu Asn
130 135 140

Asn Asn Met Gly Ile His Lys Asn Ile Val Tyr Asp Asp Asn Asn Asn
145 150 155 160

Asn Lys Asn Val Thr Tyr Asp Asp Asn Asn Lys Asn Val Thr Tyr Asp
165 170 175

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Asn Asn Asn Lys Asn Val Thr Tyr Asp Asn Asn Asn Lys Asn Val Thr
            180                 185                 190

Tyr Asp Asn Asn Asn Lys Asn Val Thr Tyr Asp Asn Asn Asn Lys Asn
        195                 200                 205

Val Thr Tyr Asp Asn Asn Asn Asn Asn Ser Cys Ser Ile Ile Lys Tyr
    210                 215                 220

Glu Leu Arg Lys Thr Ser Ile Cys Lys Tyr Trp Ile Lys Gly Ile Cys
225                 230                 235                 240

Ala Asn Val Glu Cys Asn Phe Ala His Gly Glu His Glu Leu Lys Tyr
                245                 250                 255

Thr Phe Gly Val Tyr Lys Thr Thr Ile Cys Lys His Trp Lys Lys Asn
            260                 265                 270

Gly Met Cys Ser Ser Gly Ile His Cys Arg His Ala His Gly Glu Ser
        275                 280                 285

Glu Leu Gln Pro Lys Asn Leu Pro Leu His Leu Leu Lys Lys Lys Asn
    290                 295                 300

Asn Leu Lys Asn Lys Asn Gln Thr Lys Ser Phe His Thr Asn Lys Glu
305                 310                 315                 320

Leu Thr Ile Asn Glu Tyr Asn Asp Arg Ser Ala Asn Asn Arg Asn Val
                325                 330                 335

Glu His Met Tyr Lys Asn Lys Val Asp Pro Leu Lys Asn Asn Asn Asn
            340                 345                 350

Asn Asn Asp Asn Ile Tyr Tyr Tyr Gly Asn Glu Glu Asn Gln Lys Asp
        355                 360                 365

Val Asn Ile Phe Arg Met Asp Thr Phe Tyr Asn Asn Ile Phe Asp Ser
    370                 375                 380

Arg Asn His Met Asp Lys Pro Pro Pro His Asn Ile Asn Asn Asn Asn
385                 390                 395                 400

Ser Asn Asn Asn Asn Asn Asn Asn Ile Val Ser Val Glu Gly Lys Pro
                405                 410                 415
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Ile Asn His Asn Thr Pro Asn Ile Leu Asn Asp Gly Asn Tyr Thr Asn
420 425 430

His Leu Asn His Ser Asn Tyr Ile Tyr Asn Asn Glu Lys Glu Glu Asn
435 440 445

Glu Lys Arg Asn Phe Asn Tyr Tyr Asp Thr Cys Lys Asn Ile Trp Asn
450 455 460

Tyr Gln Ile Cys Lys Asp Asp Asn Asn Leu Leu Asn Asn Asn Glu Lys
465 470 475 480

Thr Phe Phe Phe Phe Ser Asn Val Asn Asn Asn Lys Met Val Glu Cys
485 490 495

Asn Asn Met Asn Asn Ile Phe Asn Asp Ile His Lys Lys Glu Asn Thr
500 505 510

Ile Thr Leu Asn Asn Asn Ser Asn Asn Val Ile Asn Ile Lys Lys Asn
515 520 525

Ile Ile Asp Asp Ala Asp Ile Ser Lys Val Thr Asn Val His Ile Tyr
530 535 540

Lys Asp Asp His Leu Lys Asn Thr Pro Ile Asn Asn Lys Lys Lys Glu
545 550 555 560

Thr Arg Leu Ser Gln Gly Lys Lys Asn Thr Tyr Leu Lys Val Asn Phe
565 570 575

Phe Asn Asn Lys Asn Lys Asp Asn Asn Tyr Asn Asn Asn Ile Ile Val
580 585 590

Asp Thr Asn Asn Asn Asn Asn Asn Asn Asn Val Ile Lys Asn Asp His
595 600 605

Asn Lys Ile Asn Asn Asn Asn Leu Ile Phe Gln Asn Ser Arg Phe Met
610 615 620

Asp His Thr Gly Ala Cys Asp Thr Ile Lys Ser Gly Asp Thr Thr Lys
625 630 635 640

Ser Gly Asp His Ile Lys Ser Gly Asp His Ile Lys Ser Gly Asp Thr
645 650 655

Ile Lys Asn Val Glu Asn Phe Val Asn Tyr Thr Asn Ser Asn Asn Ile

660 665 670

Ser Asn Ile Asn Ile Ser Ile Asn Cys Asn Asn Tyr Glu Lys Tyr Ile
675 680 685

Asn Asn Met Ser Phe Ile Asn Asn Lys Glu Ser Ser Asn Ile Asn Lys
690 695 700

Asp Asp Val Tyr Asn Gly Asn Met Asp Asn His Asn His His Val Asn
705 710 715 720

Asn Asn Asn Thr Leu Cys Asn Thr Ser Leu Ser Asp Leu Cys Ser Asn
725 730 735

Asn Ser Ser Glu Ser Lys Lys Gln Glu Ala Val Cys Leu Asn Lys Asn
740 745 750

Asp Thr His Asp Ile Ile Lys Asn Val Ser Asn Asn Met Lys Arg Phe
755 760 765

Ser Leu Tyr Met Asn Pro Ile Asn Asn Asn Asn Asn Asn Asn Asn Asn
770 775 780

Asn Asn Asp Asp Thr Ser Asn Asn Val Gln Phe Ile Asn Asn Tyr Thr
785 790 795 800

Asn Asp Tyr Phe Tyr Tyr Asp Glu Lys Lys Asp Glu Glu Gln His Asn
805 810 815

Pro Tyr Asp Asn Lys Asn Asn Lys Ile Lys Gly Phe Arg Asn Ile Asn
820 825 830

Ile Arg Ile Ile Lys Lys Glu Asp Glu Gln Glu His Thr Asn Glu Lys
835 840 845

Asn Asn Thr Ile Phe Asn Lys Asn Val Asn Glu Ile Met Tyr Ser Lys
850 855 860

Glu Ile Thr Asn Met Asn Asn Ile Asn Arg Ser Ser Asp Glu Tyr Ile
865 870 875 880

Thr Asn Asn Asn Met Asp Asn Asp Asn Asn Ile Met Asn Asn Thr Leu
885 890 895

Tyr Pro Trp Lys Glu Asn Lys Phe Lys Asn Val Asp Met Leu Asn Ile
900 905 910

Tyr Lys Ile Asn Lys Asp Asp Tyr Leu His Thr Asp Ile Val Lys Asn
915 920 925

Ile Asp Cys Val Ile Ser Pro Tyr Lys Asp Pro Asn Ile Ile Met Asp
930 935 940

Arg Ile Asn Asp Asp Asn Asn Ile Asn Met Asp Asn Leu Leu Phe Thr
945 950 955 960

Tyr Asn Glu Gln Met Asn Asn His His Asn Asn Lys Lys Trp Asn Val
965 970 975

Phe Asn Asn Ser Ile Ile Leu Glu Lys Asn Glu Lys Ile Thr Asn Ser
980 985 990

Lys Lys Lys Asn Asn Tyr Lys Ile His Gln Arg Gln Asn Ile Asn Lys
995 1000 1005

Asn Val Ser Asp Asn Asn Glu Asn Ile Asn Asn Lys Asn Val Ile
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Ser Lys Asp Lys Phe Lys Ile Ile Asn Ser Tyr Ile Asp Tyr Lys
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Leu Asn Tyr His Lys Asn Asn Lys Tyr Ser Tyr Asn Asn Met Glu
1040 1045 1050

His Asn Ile Lys Asn Val Asn Glu Gln Ser Ser Ile Asn Asn Asn
1055 1060 1065

Asn Asn Asn Asn Asn Asn Ile Leu Tyr Thr Thr Thr Lys Asp Leu
1070 1075 1080

Arg Asn Asn Ile His Thr Ile Asn Phe Asn Asp Thr Lys Asn Ile
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Ile Asn Ser Asp Asp Tyr Phe Val Asp His Asn Tyr Asn Tyr Asn
1100 1105 1110

Tyr Asn Tyr Asn Tyr Asn Tyr Asn Tyr Asn Tyr Ala Tyr Asp Asn
1115 1120 1125

Ile Glu Leu Ser Asn Lys Asn Met Lys Asp Val Ile Asn Leu Tyr
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Thr Tyr Val Val Asn Lys Lys Asn Glu Lys Asn Ile Tyr Thr Ser
1145 1150 1155

Thr Asn Asn Ile Ile Cys Asn Asp Glu Tyr Ile Lys Lys Glu Asp
1160 1165 1170

Cys Gly Asp Cys Gln Met Val Glu Ser Thr Gln Met Phe Asp Glu
1175 1180 1185

Glu Ile Asn Cys Ser Pro Glu Asn Lys Ser Asn Asn Asn Asn Asn
1190 1195 1200

Ile Asn Ser Asn Asn Ile Asn Ile Asn Ser Ser Ser Ser Ser Asn
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Asn Asn Asn Asn Asn Asn Asn Tyr Tyr Tyr Asn Asp Tyr His Asp
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Asp Asp Asn Asn Asn Asn Ile Met Asn His Ser Tyr Tyr Asn His
1235 1240 1245

Ile Asn Asp Ser Tyr Tyr Tyr Gln Phe Asn Asp Leu His Ser Lys
1250 1255 1260

Glu Asn Gln Gln Lys Tyr Thr Tyr Asn Ile Asn Asn Leu Ile His
1265 1270 1275

Asn Met Lys Leu Leu Asn Thr Glu Tyr Glu Ser Pro Leu Asn Ser
1280 1285 1290

Glu Gln Glu Lys Thr Ile Leu Lys Asn Ile Ala Val Asp Arg Asn
1295 1300 1305

Asn Asn Ile Asn Ile Asn Asn Ile Thr Leu Pro Thr Leu Gln Asp
1310 1315 1320

Asn Gln Met Asn Asn Tyr Lys Lys Tyr Thr Asn Asp Leu Gly Ser
1325 1330 1335

Val Ser Glu Gly Tyr Thr Ser Thr Tyr Asn Asp Thr Leu Lys Met
1340 1345 1350

His Ser Glu Thr Phe Met Asp Ser Gln Asn Gly Met Tyr Ile Leu
1355 1360 1365

Pro Gln Tyr Val Thr Arg Glu Cys Ile Asn Ser Pro Tyr Asp Ser
1370 1375 1380

Ser Leu Phe Thr Asp Glu Asn Arg Glu Glu Lys Lys Asp Asn Lys
1385 1390 1395

Glu Arg Glu Ile Ile Gly Asn Met Leu Tyr Asp Glu His Ile Cys
1400 1405 1410

Met Asp Asp Glu Asp Leu Phe Gly Arg Ser His Leu Phe Asn Ile
1415 1420 1425

Phe Asn Asn Glu Glu Glu Ile Asp Ile Asn Gln Lys Asp Asn Tyr
1430 1435 1440

Tyr Asp Arg Asp Asp His Asn Asp Tyr His Arg Asp Asp His Asn
1445 1450 1455

Asp Tyr Asp Arg Asp Asp His Asn Asp Tyr Asp Arg Asp Asp His
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Asn Asn Tyr His Arg Asp Asp His Asn Asn His His Arg Asp Asp
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Asn Asn Asn His His Arg Asp Asp His Asn Asn His His Arg Asp
1490 1495 1500

Asp Asn Asn Asn His His Gly Asp Asp Val Ile Tyr Glu Glu Thr
1505 1510 1515

Lys Lys Thr Asp Asn Ile Glu Ile Pro Leu Lys Asp Asn Asp Ile
1520 1525 1530

Met Ile Asn Asn Ser Tyr Asn Asp Ser Leu Ile Asn Tyr Asn Lys
1535 1540 1545

Tyr Phe Val Lys Glu His Glu Tyr Asn Asn Ile Asn Asn Asn Asn
1550 1555 1560

Lys Ile Glu Glu Asn Leu Lys Ile Lys Asn Ser Tyr Asp Thr Ser
1565 1570 1575

Ser Lys Gln Asn Tyr Lys Glu Asn Asn Met Phe His Asp Val Asp
1580 1585 1590

Asn Phe Thr Ser Leu Leu Leu His Ile Asn Asn Tyr Asn Glu Lys

1595 1600 1605

Asp Phe Met Asn Phe Lys Asn Glu Asp Tyr Thr Leu Asn Lys Glu
1610 1615 1620

Ile Tyr Phe Asn Glu Cys Lys Tyr Val Lys Glu Ile Lys Asn Ile
1625 1630 1635

Asp Gln Asp Asn Thr Lys Glu Leu Gly Ile Val Leu Gln Asn Asp
1640 1645 1650

Asp Gln Ile Ser Glu Ser Asp Met Arg Thr Lys Lys Met Ile Tyr
1655 1660 1665

Ser Ile Phe Ile Lys Glu Glu Glu Thr Lys Lys Asn Lys Asn Leu
1670 1675 1680

Glu Asn Ile Cys Tyr Thr Asn Glu Gln Glu Lys Tyr Asn Asn Leu
1685 1690 1695

Ser Ile Ile Asn Gln Lys Gln Asn Ile Thr Met Asp Ile Ile Lys
1700 1705 1710

Asn Val Asp Glu Leu Ser Phe Asp Asn Met Glu Gln Met Asn Ile
1715 1720 1725

Lys Ile Asn Asp Asn Gln Met Tyr Asn Glu Gln Val Met Asp Asn
1730 1735 1740

Met Glu Asp Arg Ile Glu Lys Ile Asn Ile Leu Thr Asn Asp Asn
1745 1750 1755

Ile Gln Asn Gly Ile His Asn Asn Asn Asn Asn Ile Ile Glu Glu
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Lys Gln Ser Leu Lys Asp Asn Asn
1775 1780

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Glu Asn Tyr Leu Asn Ala Leu Thr Asp Asp Thr Met Asn Glu Thr Val
35 40 45

Phe Leu Asp Tyr Val Lys Gly Lys Met Met Asp Val Tyr Lys Glu Thr
50 55 60

Asn Met Asn Arg Tyr Asn Val Ile Asn His Ile Tyr Leu Thr Ser Lys
65 70 75 80

Val Trp Asp Thr Tyr Asn Tyr Leu Thr Pro Thr Leu Lys Val Lys Arg
85 90 95

Phe Arg Val Phe Lys Asp Tyr Ser Phe Phe Ile Asp Glu Val Lys Lys
100 105 110

Ile Tyr Glu Asn Lys Leu Lys Lys Ser Thr Ile Cys Asn Lys Ala Ile
115 120 125

Leu Ile Asn Arg Asn Lys Asn Val Glu Met Lys Lys Gly Leu Asn Asp
130 135 140

Lys Asn Glu Thr Ser Glu Lys Lys Val Glu Glu Asn Ile Lys Asn Arg
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Lys Cys Gln Asn Glu Val Lys Glu Tyr Ser Lys Lys Asp Thr Arg Leu
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Asn Val His Asn Val Lys Glu Leu Glu Arg Asn Lys
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Ile Ser Ile Phe Cys Asn Leu Arg Arg Asn Val Phe Ser Asn Phe Asn

35 40 45

Arg Asn Asp Leu Ile Asp Gln Asn Ile Val Tyr Leu Asn Val Cys Asn
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Asn Glu Thr Tyr Tyr Asn Lys Ala His Glu Glu Asn Asp Lys Val Lys
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Leu Lys Lys Ile Leu Leu Asn Leu Asp Val Leu Ile Asp Val Ser Lys
35 40 45

Ile Val Ile Gln Lys Asn Glu Asn Phe Asp Met Glu Leu Leu Asn Asn
50 55 60

Val Asn Asp Arg Phe Val Glu Lys Ile Tyr Tyr Leu Leu Lys Asp Lys
65 70 75 80

Lys Lys Asn Met Leu Pro Glu Glu Glu Leu Val Glu Phe Ile Phe Leu
85 90 95

Leu Leu Lys Glu Arg Asn Glu Tyr Asn Asn Leu Glu Lys Lys Lys Lys
100 105 110

Asn Ile Tyr Ile Asn Val Gln Lys Asn Leu Thr Asn Cys Pro Ile Lys
115 120 125

Asn Glu Val Thr Thr Leu Ile Gln Lys Ile Asn Lys Phe Tyr Tyr Tyr
130 135 140

Phe Lys Glu Phe Leu Leu Lys Glu Lys Tyr Asn Thr Lys Asp Asp Ala
145 150 155 160

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Asn Lys Lys Tyr His His Asn Lys Glu Asp Thr Asn Asn Tyr Asn Asn
                165                 170                 175

Ile Pro Glu Asn Tyr Lys Asn Gln Ser Lys His Asn His Asp Tyr Leu
            180                 185                 190

Asn Tyr His Lys Asp Asn Ile Ile Asn Ile Asp Ile Asn Asp Leu Gly
        195                 200                 205

Tyr Asn Asn Asn Asp Asn Asn Lys Glu Ser Val Phe Tyr Asn Lys Glu
    210                 215                 220

Ile Ile Lys Asn Asn Lys Gln Arg Asn His Phe Gln Gly Lys Glu Lys
225                 230                 235                 240

Lys Asn Thr Lys Asp Glu Val Ala Thr Thr Ile His Asn Ile Leu Ser
                245                 250                 255

Cys Lys Asp Ile Ser Ser Asn Gln Phe Asn Asn Tyr Asn Asn Thr Leu
            260                 265                 270

Gln Thr Ser Asp Tyr Asn Lys Asp Phe Leu Tyr Lys Asp Val Leu Met
        275                 280                 285

Asp Ile Met Ser Thr Asp Ser Glu Lys Asn Met Thr Ser Gln Lys Ser
    290                 295                 300

Ile Thr Ser Glu Lys Asn Met Thr Cys Glu Lys Asn Met Thr Cys Glu
305                 310                 315                 320

Lys Asn Ile Thr Cys Glu Lys Asn Ile Thr Cys Glu Lys Asn Ile Thr
                325                 330                 335

Cys Glu Lys Asn Ile Thr Cys Glu Lys Asn Ile Thr Cys Glu Lys Asn
            340                 345                 350

Ile Thr Cys Glu Lys Asn Ile Thr Cys Glu Lys Asn Ile Thr Cys Glu
        355                 360                 365

Lys Asn Ile Thr Cys Asp Lys Asn Ile Ile Ile Ser Lys Arg Lys Asp
    370                 375                 380

Asn Gln Gln Thr Phe Cys Glu Asp Lys Ile Ser Val Ser Ser Asp Asp
385                 390                 395                 400
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Ile Glu Pro Leu Ile Ser Ser Tyr Ser Glu Tyr Ile Met Arg Asp Glu
405 410 415

Pro Thr Tyr Ile Pro Asp Lys Lys Leu Leu Ser Glu Glu Glu Asn Lys
420 425 430

Lys Leu Glu Lys Glu His Cys His Met Lys Asn Asn Ile Lys His Asn
435 440 445

Asp Ile Ala His Val Thr Asn Asn Asp Ser Ile Asn Asn Tyr Leu Tyr
450 455 460

Asn Lys Tyr Tyr Ile Asn Glu Asp Asn Lys Ile Met Gln Asn Asp Ser
465 470 475 480

Asn Leu Asn His Asn Lys Asn Glu Asp Ile Lys Lys Val Asp Ile Glu
485 490 495

Asn Thr His Met Ile Asn Gly Tyr Asp Pro Asn Glu Asp Ile Leu Trp
500 505 510

Asn Asn Asn Lys Thr Ile Ser Ser Glu Lys Leu Cys Val Pro Arg Thr
515 520 525

Lys Asp Asn Glu Ile Leu Lys Asn Lys Glu Leu Asn Asn Tyr Leu Gly
530 535 540

Glu Ala Tyr Asn Asp Cys Ile Asn Glu Glu Thr Tyr Lys Asn Met Lys
545 550 555 560

Leu Glu Asn Cys Asp Glu Lys Lys Lys Lys Thr Asn Phe Gln Asn Val
565 570 575

Asn Ser Asn Phe Lys Glu Gln His Leu Leu Phe Cys Asn Asn Leu Gln
580 585 590

Glu Gln Met Lys Tyr Arg Ser Asp Lys Asn Leu Lys Tyr Asp Glu Lys
595 600 605

Leu Tyr Asn Asn Asn Ile Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
610 615 620

Asn Asn Asn Thr Asn Asp Asp Ile Lys Ile Val Lys Pro Asn Asn Gln
625 630 635 640

His His Ile His Asn Asn Leu Leu His Tyr Ile Asn Asn Lys His Asn

645 650 655

Leu Leu Asn Ser Ile Thr Leu Ser Asn Ser Leu Pro Gln Lys Asn Asp
660 665 670

Tyr Gln Ile Asn Asn Phe Ile His Lys Asn Asp Thr Asn Glu Phe Lys
675 680 685

Asn Leu Thr Ile Asn Asn Phe Gln Lys Lys Glu Lys Glu Leu Tyr Thr
690 695 700

Leu Asn His Met Asn Thr Ile Lys Ser Asn Ile Asn Asn Ile His Met
705 710 715 720

Lys Asp Ser Gly Asp Thr Glu Val Thr His Asn Asn Gln Ser Phe Phe
725 730 735

Phe Asn Thr Asn Gln Ile Glu Asn Glu Lys Lys Lys Lys Asn Asn Asn
740 745 750

Asn Asn Ile Lys Thr His Ile Ala Asn Phe Asn Ile Ile His Lys Asn
755 760 765

Asn Leu Asn Glu Ser Gly Lys Asn Met Glu His Tyr Ile Ala Ser Gln
770 775 780

Glu Glu Asn Ile Leu Phe Glu Asn Lys Asn Asn Asp Met Glu Glu Leu
785 790 795 800

Tyr Arg Glu His Ser Arg Glu Leu Leu Glu Glu Asn Ile Ile Asn Lys
805 810 815

Ile Gly Asn Asn Thr Lys Lys Lys Lys Glu Tyr Asp Glu Cys Thr Met
820 825 830

Ser Thr Cys Ile Asp Asn Val Val Tyr Asn Ser His Asp Asn Ile Asn
835 840 845

Gly Glu Lys Lys Asp Glu Asn Asn Met Glu Tyr Phe Ile Lys Ser Glu
850 855 860

Asp Glu Ser Leu Lys Asp Phe Asp Met Leu Leu Tyr Asn Asn Arg Lys
865 870 875 880

Glu Asn Ser Glu Arg Glu Glu Asp Lys Ser Ile Glu Asn Ile Lys Met
885 890 895

Leu Gly Thr Glu Ser Phe Tyr Glu Asp Glu Asn Asn Asp Glu Asp Ile
900 905 910

Lys Gln Phe Asp Glu Asn Leu Thr Tyr Glu Gln Arg Lys Ile Asn Asp
915 920 925

Asp Asn Tyr Gly Asp Met His Tyr Ile Asp Val Glu Asp Asp Asp Tyr
930 935 940

Glu Asn Val Arg Asn Lys Asn Glu Asp Ser Ser Asn Ile Tyr Asp Asp
945 950 955 960

Glu Glu Ile Tyr Asn Gln Lys Glu Glu His Asp Gly Lys Lys Ile Phe
965 970 975

Leu Asn Arg Ile Glu Asn Asn Ala Ile Asn Asn Leu Tyr Lys Thr Tyr
980 985 990

Glu Met Ile Gln Gly Asp Asn Asp Asp Met Asp Asp Asn Tyr Tyr Leu
995 1000 1005

Tyr Asp Glu Asn Glu Lys Gly Ala Thr Lys Asn Ile Leu Cys Glu
1010 1015 1020

Phe Asn Lys Lys Gly Lys Lys Gly Ile Val Asn Lys Phe Asn Arg
1025 1030 1035

Asp Met Leu Gln Lys Ile Glu Lys Asn Tyr Asp Asn Asn Asp Ile
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Asn Asn Asp Asn Asn Asn Asn Asp Asn Asn Asn Asn Asn Asp Asn
1055 1060 1065

Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
1070 1075 1080

Asn Gln Lys Lys Phe Met Asn Thr Arg Asn Asp Asn Tyr Ile Asn
1085 1090 1095

Asn Asn Ile Tyr Leu Asn Lys Ala Asn Pro Asn Ile Phe Asn Glu
1100 1105 1110

Asn Thr Thr Asn Tyr Asn Gln Lys Glu Asn Ser Phe Asn Gln Ser
1115 1120 1125

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Asp Phe Leu Leu Leu Lys Lys Lys Glu Gln Gly Asn Ser Arg Leu
    1130                1135                1140

Lys Lys Trp Leu Cys Lys Ile Asn Ala Arg Glu Lys Glu Lys Glu
    1145                1150                1155

Lys Lys Leu Gln Gln Lys Lys Asn Glu Ser Tyr Asp Arg Glu Leu
    1160                1165                1170

Lys Asn Cys Thr Phe His Pro Thr Leu Asn Asn Asn Arg Ile Lys
    1175                1180                1185

Arg Glu Gly Thr Ile Lys Glu Met Asn Asp Thr Tyr Asp Asp Asp
    1190                1195                1200

Asp Asn Lys Asn Leu Ser Glu Asn Tyr Asp Cys Tyr Asn Lys Tyr
    1205                1210                1215

Val Asn Asp Thr Tyr Tyr Gly Asp Asn Asn Lys Asp Cys Tyr Asn
    1220                1225                1230

Phe Asp Gln Glu Lys Ile Tyr Asp Phe Asn Asn Asn Ser Tyr Tyr
    1235                1240                1245

Lys Asn Asn Glu Gln Asn His Ser Phe His His Phe Asn Ile Asp
    1250                1255                1260

Lys Lys Arg Asn Asp Asn Thr Asn Met Lys Lys Lys Met Asn Arg
    1265                1270                1275

Asn Lys Ile Leu Tyr Leu Lys Gly Leu Lys Ser Lys Glu Leu Leu
    1280                1285                1290

Leu Gln Lys Lys Ile Asp Tyr Gln Asn Glu Glu Glu Lys Lys Phe
    1295                1300                1305

Lys Lys Glu Cys Ile Phe His Pro Thr Ile Lys Asp Asn Val Lys
    1310                1315                1320

Ile Phe Leu Ser Asp Leu Pro Asn Gly Tyr Asn Lys Thr Val Asp
    1325                1330                1335

Arg Ile Lys Arg Gly Val Glu Glu Lys Lys Arg Ile Asn Asn Phe
    1340                1345                1350
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Leu Gln Tyr Arg Ile Pro His Met Asn Asn Asn Gly Asn Ile Gln
1355 1360 1365

Asn Glu Lys Lys Asn Glu Gly Lys Gln Asn Asn Lys Lys Lys Thr
1370 1375 1380

Asn Asn Ile Pro Gln Pro Phe Ser Phe Asp Lys Gly Gln Tyr Lys
1385 1390 1395

Val Lys Ile Lys Pro Val Phe Phe Glu Arg Lys Ile Lys Ile Ser
1400 1405 1410

Glu Asn Lys Ile Ala Cys Leu Ala Val Arg Glu Asp Glu Asp Pro
1415 1420 1425

Leu Tyr Ile Val Asp Ile Phe Cys Lys Ile His Ala Leu Lys Asn
1430 1435 1440

Glu Asn Lys Gln Ile Leu Tyr Asp Tyr Ile Leu Asp Glu Leu Lys
1445 1450 1455

Gln Glu Ser Phe Glu Lys
1460